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(54) Title: DELTA-ENDOTOXIN GENES AND METHODS FOR THEIR USE

(57) Abstract: Compositions and methods for conferring pesticidal activity to bacteria, plants, plant cells, tissues and seeds are provided. Compositions comprising a coding sequence for a delta-endotoxin and delta-endotoxin-associated polypeptides are provided. The coding sequences can be used in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. Compositions also comprise transformed bacteria, plants, plant cells, tissues, and seeds. In particular, isolated delta-endotoxin and delta-endotoxin-associated nucleic acid molecules are provided. Additionally, amino acid sequences corresponding to the polynucleotides are encompassed. In particular, the present invention provides for isolated nucleic acid molecules comprising nucleotide sequences encoding the amino acid sequences shown in in SEQ ID NOS:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, and 29, and the nucleotide sequences set forth in SEQ ID NOS:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, and 28, as well as variants and fragments thereof.



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DELTA-ENDOTOXIN GENES AND METHODS FOR THEIR USE

FIELD OF THE INVENTION

This invention relates to the field of molecular biology. Provided are novel genes that encode pesticidal proteins. These proteins and the nucleic acid sequences that encode them are useful in preparing pesticidal formulations and in the production of transgenic pest-resistant plants.

BACKGROUND OF THE INVENTION

Bacillus thuringiensis is a Gram-positive spore forming soil bacterium characterized by its ability to produce crystalline inclusions that are specifically toxic to certain orders and species of insects, but are harmless to plants and other non-targeted organisms. For this reason, compositions including *Bacillus thuringiensis* strains or their insecticidal proteins can be used as environmentally acceptable insecticides to control agricultural insect pests or insect vectors for a variety of human or animal diseases.

Crystal (Cry) proteins (delta-endotoxins) from *Bacillus thuringiensis* have potent insecticidal activity against predominantly Lepidopteran, Dipteran, and Coleopteran larvae. These proteins also have shown activity against Hymenoptera, Homoptera, Phthiraptera, Mallophaga, and Acari pest orders, as well as other invertebrate orders such as Nemathelminthes, Platyhelminthes, and Sarcomastigophora (Feitelson (1993) The *Bacillus Thuringiensis* family tree. In Advanced Engineered Pesticides. Marcel Dekker, Inc., New York, N.Y.) These proteins were originally classified as CryI to CryV based primarily on their insecticidal activity. The major classes were Lepidoptera-specific (I), Lepidoptera- and Diptera-specific (II), Coleoptera-specific (III), Diptera-specific (IV), and nematode-specific (V) and (VI). The proteins were further classified into subfamilies; more highly related proteins within each family were assigned divisional letters such

as Cry1A, Cry1B, Cry1C, etc. Even more closely related proteins within each division were given names such as Cry1C1, Cry1C2, etc.

A new nomenclature was recently described for the Cry genes based upon amino acid sequence homology rather than insect target specificity (Crickmore *et al.* (1998) *Microbiol. Mol. Biol. Rev.* 62:807-813). In the new classification, each toxin is assigned a unique name incorporating a primary rank (an Arabic number), a secondary rank (an uppercase letter), a tertiary rank (a lowercase letter), and a quaternary rank (another Arabic number). In the new classification, Roman numerals have been exchanged for Arabic numerals in the primary rank. Proteins with less than 45% sequence identity have different primary ranks, and the criteria for secondary and tertiary ranks are 78% and 95%, respectively.

The crystal protein does not exhibit insecticidal activity until it has been ingested and solubilized in the insect midgut. The ingested protoxin is hydrolyzed by proteases in the insect digestive tract to an active toxic molecule. (Höfte and Whiteley (1989) *Microbiol. Rev.* 53:242-255). This toxin binds to apical brush border receptors in the midgut of the target larvae and inserts into the apical membrane creating ion channels or pores, resulting in larval death.

Delta-endotoxins generally have five conserved sequence domains, and three conserved structural domains (see, for example, de Maagd *et al.* (2001) *Trends Genetics* 17:193-199). The first conserved structural domain consists of seven alpha helices and is involved in membrane insertion and pore formation. Domain II consists of three beta-sheets arranged in a Greek key configuration, and domain III consists of two antiparallel beta-sheets in 'jelly-roll' formation (de Maagd *et al.* (2001) *supra*). Domains II and III are involved in receptor recognition and binding, and are therefore considered determinants of toxin specificity.

Because of the devastation that insects can confer, there is a continual need to discover new forms of *Bacillus thuringiensis* delta-endotoxins.

SUMMARY OF INVENTION

Compositions and methods for conferring pesticide resistance to bacteria, plants, plant cells, tissues, and seeds are provided. Compositions include isolated nucleic acid molecules encoding sequences for delta-endotoxin and delta-endotoxin-associated polypeptides, vectors comprising those nucleic acid molecules, and host

cells comprising the vectors. Compositions also include isolated or recombinant polypeptide sequences of the endotoxin, compositions comprising these polypeptides, and antibodies to those polypeptides. The nucleotide sequences can be used in DNA constructs or expression cassettes for transformation and expression in organisms, including microorganisms and plants. The nucleotide or amino acid sequences may be synthetic sequences that have been designed for optimum expression in an organism, including, but not limited to, a microorganism or a plant. Compositions also comprise transformed bacteria, plants, plant cells, tissues, and seeds.

In particular, the present invention provides for isolated nucleic acid molecules comprising a nucleotide sequence encoding an amino acid sequence shown in SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, or a nucleotide sequence set forth in SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, as well as variants and fragments thereof. Nucleotide sequences that are complementary to a nucleotide sequence of the invention, or that hybridize to a sequence of the invention, are also encompassed.

Methods are provided for producing the polypeptides of the invention, and for using those polypeptides for controlling or killing a lepidopteran or coleopteran pest.

The compositions and methods of the invention are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms and compositions derived from them are desirable for agricultural purposes. The compositions of the invention are also useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

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DESCRIPTION OF FIGURES

Figure 1 shows an alignment of AXMI-004 (SEQ ID NO:3) with cry1Ac (SEQ ID NO:31), cry1Ca (SEQ ID NO:32), cry2Aa (SEQ ID NO:34), cry3Aa1 (SEQ ID NO:35), cry1Ia (SEQ ID NO:33), and cry7Aa (SEQ ID NO:41). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 174 to about 196 of SEQ ID NO:3. Conserved group 2 is

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found from about amino acid residue 250 to about 292 of SEQ ID NO:3. Conserved group 3 is found from about amino acid residue 476 to about 521 of SEQ ID NO:3. Conserved group 4 is found from about amino acid residue 542 to about 552 of SEQ ID NO:3. Conserved group 5 is found from about amino acid residue 618 to about 628
5 of SEQ ID NO:3

Figures 2A, B, and C show an alignment of AXMI-006 (SEQ ID NO:7) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ia (SEQ ID NO:33), cry3Aa1 (SEQ ID NO:35), cry3Ba (SEQ ID NO:36), cry 4Aa (SEQ ID NO:38), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), and cry24Aa (SEQ ID NO:47). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray.
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15 Conserved group 1 is found from about amino acid residue 218 to about 239 of SEQ ID NO:7. Conserved group 2 is found from about amino acid residue 300 to about 350 of SEQ ID NO:7. Conserved group 3 is found from about amino acid residue 547 to about 592 of SEQ ID NO:7. Conserved group 4 is found from about amino acid residue 611 to about 621 of SEQ ID NO:7. Conserved group 5 is found from about
20 amino acid residue 694 to about 704 of SEQ ID NO:7.

Figures 3A, B, and C show an alignment of AXMI-007 (SEQ ID NO:9) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ia (SEQ ID NO:33), cry3Aa1 (SEQ ID NO:35), cry3Ba (SEQ ID NO:36), cry 4Aa (SEQ ID NO:38), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), and cry24Aa (SEQ ID NO:47). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray.
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30 Conserved group 1 is found from about amino acid residue 217 to about 238 of SEQ ID NO:9. Conserved group 2 is found from about amino acid residue 299 to about 347 of SEQ ID NO:9. Conserved group 3 is found from about amino acid residue 445 to about 590 of SEQ ID NO:9. Conserved group 4 is found from about amino acid

residue 609 to about 619 of SEQ ID NO:9. Conserved group 5 is found from about amino acid residue 692 to about 702 of SEQ ID NO:9.

Figures 4A, B, and C show an alignment of AXMI-008 (SEQ ID NO:14) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ia (SEQ ID NO:33), cry2Aa (SEQ ID NO:34), cry3Aa1 (SEQ ID NO:35), cry3Bb (SEQ ID NO:37), cry4Aa (SEQ ID NO:38), cry4Ba (SEQ ID NO:39), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), cry24Aa (SEQ ID NO:47), cry25Aa (SEQ ID NO:48), cry39Aa1 (SEQ ID NO:49), and cry40Aa1 (SEQ ID NO:51). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 185 to about 206 of SEQ ID NO:14. Conserved group 2 is found from about amino acid residue 276 to about 318 of SEQ ID NO:14. Conserved group 3 is found from about amino acid residue 497 to about 547 of SEQ ID NO:14. Conserved group 4 is found from about amino acid residue 576 to about 586 of SEQ ID NO:14. Conserved group 5 is found from about amino acid residue 657 to about 667 of SEQ ID NO:14.

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Figures 5A and B show an alignment of AXMI-008orf2 (SEQ ID NO:18) with cry19Aa-orf2 (SEQ ID NO:46), crybun2-orf2 (SEQ ID NO:50), crybun3-orf2 (SEQ ID NO:52), cry4Aa (SEQ ID NO:38), and cry4Ba (SEQ ID NO:39). The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray.

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Figures 6A, B, and C show an alignment of AXMI-009 (SEQ ID NO:20) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ca (SEQ ID NO:32), cry1Ia (SEQ ID NO:33), cry3Aa1 (SEQ ID NO:35), cry3Ba (SEQ ID NO:36), cry3Bb (SEQ ID NO:37), cry4Aa (SEQ ID NO:38), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), cry24Aa (SEQ ID NO:47), cry25Aa (SEQ ID NO:48), cry40Aa1 (SEQ ID NO:51). Toxins having C-terminal non-toxic domains

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were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 196 to about 217 of SEQ ID NO:20. Conserved group 2 is found from about amino acid residue 269 to about 311 of SEQ ID NO:20. Conserved group 3 is found from about amino acid residue 514 to about 556 of SEQ ID NO:20. Conserved group 4 is found from about amino acid residue 574 to about 584 of SEQ ID NO:20. Conserved group 5 is found from about amino acid residue 651 to about 661 of SEQ ID NO:20.

Figures 7A, B, and C show an alignment of AXMI-014 (SEQ ID NO:27) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ia (SEQ ID NO:33), cry2Aa (SEQ ID NO:34), cry3Aa1 (SEQ ID NO:35), cry3Bb (SEQ ID NO:37), cry4Aa (SEQ ID NO:38), cry4Ba (SEQ ID NO:39), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), cry24Aa (SEQ ID NO:47), cry25Aa (SEQ ID NO:48), cry39Aa1 (SEQ ID NO:49), and cry40Aa1 (SEQ ID NO:51). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 177 to about 188 of SEQ ID NO:27. Conserved group 2 is found from about amino acid residue 251 to about 293 of SEQ ID NO:27. Conserved group 3 is found from about amino acid residue 483 to about 533 of SEQ ID NO:27. Conserved group 4 is found from about amino acid residue 552 to about 562 of SEQ ID NO:27.

Figure 8 shows a photograph of a 4-20% gradient SDS acrylamide gel. Lanes 1-4 contain various concentrations of sporulated *Bacillus* cell culture expressing 69 kD AXMI-004 protein. Lanes 5-8 contain various concentrations of BSA. Lane 9 contains a size marker. An arrow indicates the 69 kD band.

DETAILED DESCRIPTION

The present invention is drawn to compositions and methods for regulating pest resistance in organisms, particularly plants or plant cells. The methods involve

transforming organisms with a nucleotide sequence encoding a delta-endotoxin or delta-endotoxin-associated protein of the invention. In particular, the nucleotide sequences of the invention are useful for preparing plants and microorganisms that possess pesticidal activity. Thus, transformed bacteria, plants, plant cells, plant
5 tissues and seeds are provided. Compositions are delta-endotoxin or delta-endotoxin-associated nucleic acids and proteins of *Bacillus thuringiensis*. The sequences find use in the construction of expression vectors for subsequent transformation into organisms of interest, as probes for the isolation of other delta-endotoxin or delta-endotoxin-associated genes, and for the generation of altered pesticidal proteins by
10 methods known in the art, such as domain swapping or DNA shuffling. The proteins find use in controlling or killing lepidopteran or coleopteran pest populations and for producing compositions with pesticidal activity.

Definitions

15 By "delta-endotoxin" is intended a toxin from *Bacillus thuringiensis* that has toxic activity against one or more pests, including, but not limited to, members of the Lepidoptera, Diptera, and Coleoptera orders. In some cases, delta-endotoxin proteins have been isolated from other organisms, including *Clostridium bifermentans* and *Paenibacillus popilliae*. Delta-endotoxin proteins include amino acid sequences
20 deduced from the full-length nucleotide sequences disclosed herein, and amino acid sequences that are shorter than the full-length sequences, either due to the use of an alternate downstream start site, or due to processing that produces a shorter protein having pesticidal activity. Processing may occur in the organism the protein is expressed in, or in the pest after ingestion of the protein. Delta-endotoxins include
25 proteins identified as cry1 through cry43, cyt1 and cyt2, and Cyt-like toxin. There are currently over 250 known species of delta-endotoxins with a wide range of specificities and toxicities. For an expansive list see Crickmore *et al.* (1998), *Microbiol. Mol. Biol. Rev.* 62:807-813, and for regular updates see Crickmore *et al.* (2003) "*Bacillus thuringiensis* toxin nomenclature," at
30 www.biols.susx.ac.uk/Home/Neil_Crickmore/Bt/index.

Bacterial genes, such as the AXMI genes of this invention, quite often possess multiple methionine initiation codons in proximity to the start of the open reading frame. Often, translation initiation at one or more of these start codons will lead to

generation of a functional protein. These start codons can include ATG codons. However, bacteria such as *Bacillus sp.* also recognize the codon GTG as a start codon, and proteins that initiate translation at GTG codons contain a methionine at the first amino acid. Furthermore, it is not often determined *a priori* which of these codons are used naturally in the bacterium. Thus, it is understood that use of one of the alternate methionine codons may also lead to generation of delta-endotoxin proteins that encode pesticidal activity. For example, an alternate start site for an AXMI-004 delta-endotoxin protein of the invention is at base pair 385 of SEQ ID NO:1. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:5. An alternate start site for an AXMI-007 delta-endotoxin protein of the invention may be at base pair 151 of SEQ ID NO:8. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:11. An alternate start site for an AXMI-008 delta-endotoxin protein of the invention may be at nucleotide 177 of SEQ ID NO:12. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:16. An alternate start site for an AXMI-009 delta-endotoxin protein of the invention may be at nucleotide 34 of SEQ ID NO:19. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:22. An additional alternate start site for an AXMI-009 delta-endotoxin protein of the invention may be at nucleotide 64 of SEQ ID NO:1. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:24. An alternate start site for an AXMI-014 delta-endotoxin protein of the invention may be at base pair 136 of SEQ ID NO:25. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:29. These delta-endotoxin proteins are encompassed in the present invention and may be used in the methods of the present invention.

In addition, there may be one or more additional open reading frames in the disclosed nucleotide sequences that encode one or more delta-endotoxin-associated proteins. By "delta-endotoxin-associated protein" is intended a protein encoded by a nucleotide sequence disclosed herein using an alternate open reading frame than that used by the delta-endotoxins of the present invention. Proteins such as these are known in the art as helper proteins, stabilizing sequences, or delta-endotoxin-associated proteins. These delta-endotoxin-associated proteins may have pesticidal activity, or may be important in facilitating expression of delta-endotoxin proteins.

Methods are known in the art for measuring pesticidal activity and for determining the effects of delta-endotoxin-associated proteins on delta-endotoxin protein expression and crystal formation (see, for example, Park *et al.* (1999) *FEMS Microbiol. Lett.* 181:319-327; Ge *et al.* (1998) *FEMS Microbiol. Lett.* 165:35-41; Rosso and Delecluse (1997) *Appl. Environ. Microbiol.* 63:4449-4455). These delta-endotoxin-associated proteins are encompassed by the present invention, and may be used in the methods disclosed herein, either alone or in combination with known delta-endotoxin proteins. In one embodiment, the delta-endotoxin-associated protein has the amino acid sequence found in SEQ ID NO:18 and is encoded by the nucleotide sequence of SEQ ID NO:17.

By "plant cell" is intended all known forms of plant, including undifferentiated tissue (e.g. callus), suspension culture cells, protoplasts, leaf cells, root cells, phloem cells, plant seeds, pollen, propagules, embryos and the like. By "plant expression cassette" is intended a DNA construct that is capable of resulting in the expression of a protein from an open reading frame in a plant cell. Typically these contain a promoter and a coding sequence. Often, such constructs will also contain a 3' untranslated region. Such constructs may contain a 'signal sequence' or 'leader sequence' to facilitate co-translational or post-translational transport of the peptide to certain intracellular structures such as the chloroplast (or other plastid), endoplasmic reticulum, or Golgi apparatus.

By "signal sequence" is intended a sequence that is known or suspected to result in cotranslational or post-translational peptide transport across the cell membrane. In eukaryotes, this typically involves secretion into the Golgi apparatus, with some resulting glycosylation. By "leader sequence" is intended any sequence that when translated, results in an amino acid sequence sufficient to trigger co-translational transport of the peptide chain to a sub-cellular organelle. Thus, this includes leader sequences targeting transport and/or glycosylation by passage into the endoplasmic reticulum, passage to vacuoles, plastids including chloroplasts, mitochondria, and the like.

By "plant transformation vector" is intended a DNA molecule that is necessary for efficient transformation of a plant cell. Such a molecule may consist of one or more plant expression cassettes, and may be organized into more than one 'vector' DNA molecule. For example, binary vectors are plant transformation vectors

that utilize two non-contiguous DNA vectors to encode all requisite cis- and trans-acting functions for transformation of plant cells (Hellens and Mullineaux (2000) *Trends in Plant Science* 5:446-451). "Vector" refers to a nucleic acid construct designed for transfer between different host cells. "Expression vector" refers to a
5 vector that has ability to incorporate, integrate and express heterologous DNA sequences or fragments in a foreign cell.

"Transgenic plants" or "transformed plants" or "stably transformed plants or cells or tissues" refers to plants that have incorporated or integrated exogenous nucleic acid sequences or DNA fragments into the plant cell. These nucleic acid
10 sequences include those that are exogenous, or not present in the untransformed plant cell, as well as those that may be endogenous, or present in the untransformed plant cell. "Heterologous" generally refers to the nucleic acid sequences that are not endogenous to the cell or part of the native genome in which they are present, and have been added to the cell by infection, transfection, microinjection, electroporation,
15 microprojection, or the like.

"Promoter" refers to a nucleic acid sequence that functions to direct transcription of a downstream coding sequence. The promoter together with other transcriptional and translational regulatory nucleic acid sequences (also termed "control sequences") are necessary for the expression of a DNA sequence of interest.

20 Provided herein are novel isolated nucleotide sequences that confer pesticidal activity. Also provided are the amino acid sequences for the delta-endotoxin and delta-endotoxin-associated proteins. The protein resulting from translation of this gene allows cells to control or kill pests that ingest it.

An "isolated" or "purified" nucleic acid molecule or protein, or biologically
25 active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the
30 nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For purposes of the invention, "isolated" when used to refer to nucleic acid molecules excludes isolated chromosomes. For example, in various embodiments, the isolated delta-endotoxin or delta-endotoxin-associated-encoding nucleic acid

molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequence that naturally flanks the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A delta-endotoxin or delta-endotoxin-associated protein that is substantially free of cellular material includes
5 preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of non-delta-endotoxin or non-delta-endotoxin-associated protein (also referred to herein as a "contaminating protein"). Various aspects of the invention are described in further detail in the following subsections.

10 Isolated Nucleic Acid Molecules, and Variants and Fragments Thereof

One aspect of the invention pertains to isolated nucleic acid molecules comprising nucleotide sequences encoding delta-endotoxin or delta-endotoxin-associated proteins and polypeptides or biologically active portions thereof, as well as nucleic acid molecules sufficient for use as hybridization probes to identify delta-
15 endotoxin or delta-endotoxin-associated-encoding nucleic acids. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

20 Nucleotide sequences encoding the proteins of the present invention include the sequences set forth in SEQ ID NOS:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, and 28, and complements thereof. By "complement" is intended a nucleotide sequence that is sufficiently complementary to a given nucleotide sequence such that it can hybridize to the given nucleotide sequence to thereby form a stable duplex. The
25 corresponding amino acid sequences for the delta-endotoxin or delta-endotoxin-associated proteins encoded by these nucleotide sequences are set forth in SEQ ID NOS:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, and 29.

Nucleic acid molecules that are fragments of these delta-endotoxin or delta-endotoxin-associated protein-encoding nucleotide sequences are also encompassed by
30 the present invention. By "fragment" is intended a portion of the nucleotide sequence encoding a delta-endotoxin protein or delta-endotoxin-associated protein. A fragment of a nucleotide sequence may encode a biologically active portion of a delta-endotoxin or delta-endotoxin-associated protein, or it may be a fragment that can be

used as a hybridization probe or PCR primer using methods disclosed below. Nucleic acid molecules that are fragments of a delta-endotoxin or a delta-endotoxin-associated nucleotide sequence comprise at least about 15, 20, 50, 75, 100, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 3000, 3500, 4000, 4500, 5000, 5500 nucleotides, or up to the number of nucleotides present in a full-length delta-endotoxin or delta-endotoxin-associated protein-encoding nucleotide sequence disclosed herein (for example, 2190 nucleotides for SEQ ID NO:1, 1890 for SEQ ID NO:2, etc.), depending upon the intended use.

10 Fragments of the nucleotide sequences of the present invention will encode protein fragments that retain the biological activity of the delta endotoxin or delta-endotoxin-associated protein and, hence, retain pesticidal activity or delta-endotoxin-associated protein activity, respectively. By "delta-endotoxin activity" is intended pesticidal activity. By "delta-endotoxin-associated protein activity" is intended that
15 the protein have pesticidal activity, or that the protein improves expression of a delta-endotoxin protein. This improvement in protein expression can happen by any mechanism. By "retains activity" is intended that the fragment will have at least about 30%, preferably at least about 50%, more preferably at least about 70%, even more preferably at least about 80% of the activity of the delta-endotoxin or delta-endotoxin-associated protein. Methods are known in the art for determining the effects of delta-endotoxin-associated proteins on delta-endotoxin protein expression and crystal
20 formation (see, for example, Park *et al.* (1999) *FEMS Microbiol. Lett.* 181:319-327; Ge *et al.* (1998) *FEMS Microbiol. Lett.* 165:35-41; Rosso and Delecluse (1997) *Appl. Environ. Microbiol.* 63:4449-4455). Methods for measuring pesticidal activity are
25 well known in the art. See, for example, Czapla and Lang (1990) *J. Econ. Entomol.* 83(6): 2480-2485; Andrews *et al.* (1988) *Biochem. J.* 252:199-206; Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293; and U.S. Patent No. 5,743,477, all of which are herein incorporated by reference in their entirety.

 A fragment of a delta-endotoxin or delta-endotoxin-associated protein-
30 encoding nucleotide sequence that encodes a biologically active portion of a protein of the invention will encode at least about 15, 25, 30, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 550, 600, or 650 contiguous amino acids, or up to the total number of amino acids present in a full-length delta-endotoxin or delta-

endotoxin-associated protein of the invention (for example, 629 amino acids for SEQ ID NO:3, 601 amino acids for SEQ ID NO:5, etc.).

Preferred delta-endotoxin or delta-endotoxin-associated proteins of the present invention are encoded by a nucleotide sequences sufficiently identical to the
5 nucleotide sequences of in SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29. By "sufficiently identical" is intended an amino acid or nucleotide sequence that has at least about 60% or 65% sequence identity, preferably about 70% or 75% sequence identity, more preferably about 80% or 85% sequence identity, most preferably about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity
10 compared to a reference sequence using one of the alignment programs described herein using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like.

15 To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., percent identity = number of identical positions/total number of positions (e.g., overlapping positions) x 100). In one
20 embodiment, the two sequences are the same length. The percent identity between two sequences can be determined using techniques similar to those described below, with or without allowing gaps. In calculating percent identity, typically exact matches are counted.

The determination of percent identity between two sequences can be
25 accomplished using a mathematical algorithm. A nonlimiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul *et al.*
30 (1990) *J. Mol. Biol.* 215:403. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to delta-endotoxin or delta-endotoxin-associated nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTX

program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to delta-endotoxin or delta-endotoxin-associated protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-
5 Blast can be used to perform an iterated search that detects distant relationships between molecules. See, Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) can be used. See, www.ncbi.nlm.nih.gov. Another non-limiting example of a mathematical algorithm utilized for the
10 comparison of sequences is the ClustalW algorithm (Higgins *et al.* (1994) *Nucleic Acids Res.* 22:4673-4680). ClustalW compares sequences and aligns the entirety of the amino acid or DNA sequence, and thus can provide data about the sequence conservation of the entire amino acid sequence. The ClustalW algorithm is used in several commercially available DNA/amino acid analysis software packages, such as
15 the ALIGNX module of the vector NTi Program Suite (Informax, Inc). After alignment of amino acid sequences with ClustalW, the percent amino acid identity can be assessed. A non-limiting example of a software program useful for analysis of ClustalW alignments is GeneDoc™. Genedoc™ (Karl Nicholas) allows assessment of amino acid (or DNA) similarity and identity between multiple proteins. Another non-
20 limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0), which is part of the GCG sequence alignment software package (available from Accelrys, Inc., 9865 Scranton Rd., San Diego, California, USA). When utilizing the ALIGN program for
25 comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

The invention also encompasses variant nucleic acid molecules. "Variants" of the delta-endotoxin or delta-endotoxin-associated protein-encoding nucleotide sequences include those sequences that encode the delta-endotoxin or delta-
30 endotoxin-associated proteins disclosed herein but that differ conservatively because of the degeneracy of the genetic code as well as those that are sufficiently identical as discussed above. Naturally occurring allelic variants can be identified with the use of well-known molecular biology techniques, such as polymerase chain reaction (PCR)

and hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences that have been generated, for example, by using site-directed mutagenesis but which still encode the delta-endotoxin or delta-endotoxin-associated proteins disclosed in the present invention as discussed below. Variant proteins encompassed by the present invention are biologically active, that is they continue to possess the desired biological activity of the native protein, that is, retaining pesticidal activity. By "retains activity" is intended that the variant will have at least about 30%, preferably at least about 50%, more preferably at least about 70%, even more preferably at least about 80% of the activity of the delta-endotoxin or delta-endotoxin-associated protein. Methods for measuring pesticidal activity are well known in the art. See, for example, Czapla and Lang (1990) *J. Econ. Entomol.* 83(6): 2480-2485; Andrews *et al.* (1988) *Biochem. J.* 252:199-206; Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293; and U.S. Patent No. 5,743,477, all of which are herein incorporated by reference in their entirety.

The invention also encompasses variant nucleic acid molecules. "Variants" of the delta-endotoxin or delta-endotoxin-associated-encoding nucleotide sequences include those sequences that encode the delta-endotoxin or delta-endotoxin-associated proteins disclosed herein but that differ conservatively because of the degeneracy of the genetic code as well as those that are sufficiently identical as discussed above. Naturally occurring allelic variants can be identified with the use of well-known molecular biology techniques, such as polymerase chain reaction (PCR) and hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences that have been generated, for example, by using site-directed mutagenesis but which still encode the delta-endotoxin or delta-endotoxin-associated proteins disclosed in the present invention as discussed below.

The skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences of the invention thereby leading to changes in the amino acid sequence of the encoded delta-endotoxin or delta-endotoxin-associated proteins, without altering the biological activity of the proteins. Thus, variant isolated nucleic acid molecules can be created by introducing one or more nucleotide substitutions, additions, or deletions into the corresponding nucleotide sequence

disclosed herein, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Such variant nucleotide sequences are also encompassed by the present invention.

For example, preferably, conservative amino acid substitutions may be made at one or more predicted, preferably nonessential amino acid residues. A "nonessential" amino acid residue is a residue that can be altered from the wild-type sequence of a delta-endotoxin or delta-endotoxin-associated protein without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

There are generally five highly conserved regions among the delta-endotoxin proteins, concentrated largely in the center of the domain or at the junction between domains (Rajamohan *et al.* (1998) *Prog. Nucleic Acid Res. Mol. Biol.* 60:1-23). The blocks of conserved amino acids for various delta-endotoxins as well as consensus sequences may be found in Schnepf *et al.* (1998) *Microbio. Mol. Biol. Rev.* 62:775-806 and Lereclus *et al.* (1989) *Role, Structure, and Molecular Organization of the Genes Coding for the Parasporal d-endotoxins of Bacillus thuringiensis. In Regulation of Prokaryotic Development.* Issar Smit, Slepecky, R.A., Setlow, P. American Society for Microbiology, Washington, D.C. 20006. It has been proposed that delta-endotoxins having these conserved regions may share a similar structure, consisting of three domains (Li *et al.* (1991) *Nature* 353: 815-821). Domain I has the highest similarity between delta-endotoxins (Bravo (1997) *J. Bacteriol.* 179:2793-2801).

Amino acid substitutions may be made in nonconserved regions that retain function. In general, such substitutions would not be made for conserved amino acid residues, or for amino acid residues residing within a conserved motif, where such residues are essential for protein activity. Examples of residues that are conserved and that may be essential for protein activity include, for example, residues that are identical between all proteins contained in the alignments provided. Examples of residues that are conserved but that may allow conservative amino acid substitutions and still retain activity include, for example, residues that have only conservative substitutions between all proteins contained in the alignments provided. However, one of skill in the art would understand that functional variants may have minor conserved or nonconserved alterations in the conserved residues.

Alternatively, variant nucleotide sequences can be made by introducing mutations randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ability to confer delta-endotoxin or delta-endotoxin-associated activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly, and the activity of the protein can be determined using standard assay techniques.

Using methods such as PCR, hybridization, and the like corresponding delta-endotoxin or delta-endotoxin-associated sequences can be identified, such sequences having substantial identity to the sequences of the invention. See, for example, Sambrook J., and Russell, D.W. (2001) *Molecular Cloning: A Laboratory Manual*. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) and Innis, *et al.* (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, NY).

In a hybridization method, all or part of the delta-endotoxin or delta-endotoxin-associated nucleotide sequence can be used to screen cDNA or genomic libraries. Methods for construction of such cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook and Russell, 2001. The so-called hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker, such as other radioisotopes, a fluorescent compound, an enzyme, or an enzyme co-factor. Probes for hybridization can be made by labeling synthetic oligonucleotides based on the known delta-endotoxin or delta-

endotoxin-associated-encoding nucleotide sequence disclosed herein. Degenerate primers designed on the basis of conserved nucleotides or amino acid residues in the nucleotide sequence or encoded amino acid sequence can additionally be used. The probe typically comprises a region of nucleotide sequence that hybridizes under
5 stringent conditions to at least about 12, preferably about 25, more preferably at least about 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 consecutive nucleotides of delta-endotoxin or delta-endotoxin-associated-encoding nucleotide sequence of the invention or a fragment or variant thereof. Preparation of probes for hybridization is generally known in the art and is disclosed in Sambrook and Russell, 2001, herein
10 incorporated by reference.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may
15 be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the delta-endotoxin or delta-endotoxin-associated sequence of the invention. Methods for preparation of probes for
20 hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

For example, the entire delta-endotoxin or delta-endotoxin-associated
25 sequence disclosed herein, or one or more portions thereof, may be used as a probe capable of specifically hybridizing to corresponding delta-endotoxin or delta-endotoxin-associated-like sequences and messenger RNAs. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique and are preferably at least about 10 nucleotides in length, and most preferably
30 at least about 20 nucleotides in length. Such probes may be used to amplify corresponding delta-endotoxin or delta-endotoxin-associated sequences from a chosen organism by PCR. This technique may be used to isolate additional coding sequences from a desired organism or as a diagnostic assay to determine the presence of coding

sequences in an organism. Hybridization techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, for example, Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

5 Hybridization of such sequences may be carried out under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in
10 different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000
15 nucleotides in length, preferably less than 500 nucleotides in length.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than
20 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency
25 conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. Duration of hybridization is generally less than about 24
30 hours, usually about 4 to about 12 hours.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl

(1984) *Anal. Biochem.* 138:267-284: $T_m = 81.5^{\circ}\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geq 90\%$ identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 (Elsevier, New York); and Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene Publishing and Wiley-Interscience, New York). See Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

30 Isolated Proteins and Variants and Fragments Thereof

Delta-endotoxin and delta-endotoxin-associated proteins are also encompassed within the present invention. By "delta-endotoxin protein" is intended a protein having the amino acid sequence set forth in SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22,

24, 27, or 29. By "delta-endotoxin-associated protein" is intended a protein having the amino acid sequence set forth in SEQ ID NO:18. Fragments, biologically active portions, and variants thereof are also provided, and may be used to practice the methods of the present invention.

5 "Fragments" or "biologically active portions" include polypeptide fragments comprising a portion of an amino acid sequence encoding a delta-endotoxin or delta-endotoxin-associated protein as set forth in SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, and that retain delta-endotoxin activity or delta-endotoxin-associated activity. A biologically active portion of a delta-endotoxin or delta-endotoxin-associated protein can be a polypeptide that is, for example, 10, 25, 50, 100
10 or more amino acids in length. Such biologically active portions can be prepared by recombinant techniques and evaluated for delta-endotoxin or delta-endotoxin-associated activity. Methods for measuring pesticidal activity are well known in the art. See, for example, Czaplak and Lang (1990) *J. Econ. Entomol.* 83(6): 2480-2485; Andrews *et al.* (1988) *Biochem. J.* 252:199-206; Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293; and U.S. Patent No. 5,743,477, all of which are herein
15 incorporated by reference in their entirety. As used here, a fragment comprises at least 8 contiguous amino acids SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29. The invention encompasses other fragments, however, such as any fragment in
20 the protein greater than about 10, 20, 30, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, and 650 amino acids.

By "variants" is intended proteins or polypeptides having an amino acid sequence that is at least about 60%, 65%, preferably about 70%, 75%, more preferably about 80%, 85%, most preferably about 90%, 91%, 92%, 93%, 94%, 95%,
25 96%, 97%, 98% or 99% identical to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29. Variants also include polypeptides encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, or a complement thereof, under stringent conditions. Such variants generally retain delta-endotoxin or delta-endotoxin-associated activity. Variants include polypeptides that differ in amino acid
30 sequence due to mutagenesis. Variant proteins encompassed by the present invention are biologically active, that is they continue to possess the desired biological activity of the native protein, that is, retaining pesticidal activity. Methods for measuring

pesticidal activity are well known in the art. See, for example, Czapla and Lang (1990) *J. Econ. Entomol.* 83(6): 2480-2485; Andrews *et al.* (1988) *Biochem. J.* 252:199-206; Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293; and U.S. Patent No. 5,743,477, all of which are herein incorporated by reference in their
5 entirety.

Altered or Improved Variants

It is recognized that DNA sequences of a delta-endotoxin or delta-endotoxin-associated protein may be altered by various methods, and that these alterations may
10 result in DNA sequences encoding proteins with amino acid sequences different than that encoded by the delta-endotoxin or delta-endotoxin-associated protein of the present invention. This protein may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the
15 delta-endotoxin or delta-endotoxin-associated protein can be prepared by mutations in the DNA. This may also be accomplished by one of several forms of mutagenesis and/or in directed evolution. In some aspects, the changes encoded in the amino acid sequence will not substantially affect the function of the protein. Such variants will possess the desired pesticidal activity. However, it is understood that the ability of a
20 delta-endotoxin or delta-endotoxin-associated protein to confer pesticidal activity may be improved by the use of such techniques upon the compositions of this invention. For example, one may express the delta-endotoxin or delta-endotoxin-associated protein in host cells that exhibit high rates of base misincorporation during DNA replication, such as XL-1 Red (Stratagene). After propagation in such strains, one can
25 isolate the delta-endotoxin or delta-endotoxin-associated DNA (for example by preparing plasmid DNA, or by amplifying by PCR and cloning the resulting PCR fragment into a vector), culture the delta-endotoxin or delta-endotoxin-associated mutations in a non-mutagenic strain, and identify mutated delta-endotoxin or delta-endotoxin-associated genes with pesticidal activity, for example by performing an
30 assay to test for pesticidal activity. Generally, the protein is mixed and used in feeding assays. See, for example Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293. Such assays can include contacting plants with one or more pests and determining the plant's ability to survive and/or cause the death of the pests.

Examples of mutations that result in increased toxicity are found in Schnepf *et al.* (1998) *Microbiol. Mol. Biol. Rev.* 62:775-806.

Alternatively, alterations may be made to the protein sequence of many proteins at the amino or carboxy terminus without substantially affecting activity.

5 This can include insertions, deletions, or alterations introduced by modern molecular methods, such as PCR, including PCR amplifications that alter or extend the protein coding sequence by virtue of inclusion of amino acid encoding sequences in the oligonucleotides utilized in the PCR amplification. Alternatively, the protein sequences added can include entire protein-coding sequences, such as those used
10 commonly in the art to generate protein fusions. Such fusion proteins are often used to (1) increase expression of a protein of interest (2) introduce a binding domain, enzymatic activity, or epitope to facilitate either protein purification, protein detection, or other experimental uses known in the art (3) target secretion or translation of a protein to a subcellular organelle, such as the periplasmic space of
15 Gram-negative bacteria, or the endoplasmic reticulum of eukaryotic cells, the latter of which often results in glycosylation of the protein.

Variant nucleotide and amino acid sequences of the present invention also encompass sequences derived from mutagenic and recombinogenic procedures such as DNA shuffling. With such a procedure, one or more different delta-endotoxin or
20 delta-endotoxin-associated protein coding regions can be used to create a new delta-endotoxin or delta-endotoxin-associated protein possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. For
25 example, using this approach, sequence motifs encoding a domain of interest may be shuffled between the delta-endotoxin or delta-endotoxin-associated gene of the invention and other known delta-endotoxin or delta-endotoxin-associated genes to obtain a new gene coding for a protein with an improved property of interest, such as an increased insecticidal activity. Strategies for such DNA shuffling are known in the
30 art. See, for example, Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751; Stemmer (1994) *Nature* 370:389-391; Crameri *et al.* (1997) *Nature Biotech.* 15:436-438; Moore *et al.* (1997) *J. Mol. Biol.* 272:336-347; Zhang *et al.* (1997) *Proc. Natl.*

Acad. Sci. USA 94:4504-4509; Crameri *et al.* (1998) *Nature* 391:288-291; and U.S. Patent Nos. 5,605,793 and 5,837,458.

Domain swapping or shuffling is another mechanism for generating altered delta-endotoxin or delta-endotoxin-associated proteins. Domains II and III may be swapped between delta-endotoxin proteins, resulting in hybrid or chimeric toxins with improved pesticidal activity or target spectrum. Methods for generating recombinant proteins and testing them for pesticidal activity are well known in the art (see, for example, Naimov *et al.* (2001) *Appl. Environ. Microbiol.* 67:5328-5330; de Maagd *et al.* (1996) *Appl. Environ. Microbiol.* 62:1537-1543; Ge *et al.* (1991) *J. Biol. Chem.* 266:17954-17958; Schnepf *et al.* (1990) *J. Biol. Chem.* 265:20923-20930; Rang *et al.* 91999) *Appl. Environ. Microbiol.* 65:2918-2925).

Plant Transformation

Transformation of plant cells can be accomplished by one of several techniques known in the art. First, one engineers the delta-endotoxin or delta-endotoxin-associated gene in a way that allows its expression in plant cells. Typically a construct that expresses such a protein would contain a promoter to drive transcription of the gene, as well as a 3' untranslated region to allow transcription termination and polyadenylation. The organization of such constructs is well known in the art. In some instances, it may be useful to engineer the gene such that the resulting peptide is secreted, or otherwise targeted within the plant cell. For example, the gene can be engineered to contain a signal peptide to facilitate transfer of the peptide to the endoplasmic reticulum. It may also be preferable to engineer the plant expression cassette to contain an intron, such that mRNA processing of the intron is required for expression.

Typically this 'plant expression cassette' will be inserted into a 'plant transformation vector'. This plant transformation vector may be comprised of one or more DNA vectors needed for achieving plant transformation. For example, it is a common practice in the art to utilize plant transformation vectors that are comprised of more than one contiguous DNA segment. These vectors are often referred to in the art as 'binary vectors'. Binary vectors as well as vectors with helper plasmids are most often used for *Agrobacterium*-mediated transformation, where the size and complexity of DNA segments needed to achieve efficient transformation is quite

large, and it is advantageous to separate functions onto separate DNA molecules. Binary vectors typically contain a plasmid vector that contains the cis-acting sequences required for T-DNA transfer (such as left border and right border), a selectable marker that is engineered to be capable of expression in a plant cell, and a
5 'gene of interest' (a gene engineered to be capable of expression in a plant cell for which generation of transgenic plants is desired). Also present on this plasmid vector are sequences required for bacterial replication. The cis-acting sequences are arranged in a fashion to allow efficient transfer into plant cells and expression therein. For example, the selectable marker gene and the gene of interest are located between the
10 left and right borders. Often a second plasmid vector contains the trans-acting factors that mediate T-DNA transfer from *Agrobacterium* to plant cells. This plasmid often contains the virulence functions (Vir genes) that allow infection of plant cells by *Agrobacterium*, and transfer of DNA by cleavage at border sequences and vir-mediated DNA transfer, as is understood in the art (Hellens and Mullineaux (2000)
15 *Trends in Plant Science*, 5:446-451). Several types of *Agrobacterium* strains (e.g. LBA4404, GV3101, EHA101, EHA105, etc.) can be used for plant transformation. The second plasmid vector is not necessary for transforming the plants by other methods such as microprojection, microinjection, electroporation, polyethylene glycol, etc.

20 In general, plant transformation methods involve transferring heterologous DNA into target plant cells (e.g. immature or mature embryos, suspension cultures, undifferentiated callus, protoplasts, etc.), followed by applying a maximum threshold level of appropriate selection (depending on the selectable marker gene) to recover the transformed plant cells from a group of untransformed cell mass. Explants are
25 typically transferred to a fresh supply of the same medium and cultured routinely. Subsequently, the transformed cells are differentiated into shoots after placing on regeneration medium supplemented with a maximum threshold level of selecting agent. The shoots are then transferred to a selective rooting medium for recovering rooted shoot or plantlet. The transgenic plantlet then grows into a mature plant and
30 produces fertile seeds (e.g. Hiei *et al.* (1994) *The Plant Journal* 6: 271-282; Ishida *et al.* (1996) *Nature Biotechnology* 14: 745-750). Explants are typically transferred to a fresh supply of the same medium and cultured routinely. A general description of the techniques and methods for generating transgenic plantlets are found in Ayres and

Park, 1994 (*Critical Reviews in Plant Science* 13: 219-239) and Bommineni and Jauhar, 1997 (*Maydica* 42: 107-120). Since the transformed material contains many cells; both transformed and non-transformed cells are present in any piece of subjected target callus or tissue or group of cells. The ability to kill non-transformed
5 cells and allow transformed cells to proliferate results in transformed plant cultures. Often, the ability to remove non-transformed cells is a limitation to rapid recovery of transformed plant cells and successful generation of transgenic plants.

Generation of transgenic plants may be performed by one of several methods, including but not limited to introduction of heterologous DNA by *Agrobacterium* into
10 plant cells (*Agrobacterium*-mediated transformation), bombardment of plant cells with heterologous foreign DNA adhered to particles, and various other non-particle direct-mediated methods (e.g. Hiei *et al.* (1994) *The Plant Journal* 6: 271-282; Ishida *et al.* (1996) *Nature Biotechnology* 14: 745-750; Ayres and Park (1994) *Critical Reviews in Plant Science* 13: 219-239; Bommineni and Jauhar (1997) *Maydica* 42:
15 107-120) to transfer DNA.

Transformation protocols as well as protocols for introducing nucleotide sequences into plants may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Suitable methods of introducing nucleotide sequences into plant cells and subsequent insertion into the plant genome
20 include microinjection (Crossway *et al.* (1986) *Biotechniques* 4:320-334), electroporation (Riggs *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606, *Agrobacterium*-mediated transformation (U.S. Patent No. 5,563,055; U.S. Patent No. 5,981,840), direct gene transfer (Paszkowski *et al.* (1984) *EMBO J.* 3:2717-2722), and ballistic particle acceleration (see, for example, U.S. Patent No. 4,945,050; U.S.
25 Patent No. 5,879,918; U.S. Patent No. 5,886,244; U.S. Patent No. 5,932,782; Tomes *et al.* (1995) "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg and Phillips (Springer-Verlag, Berlin); McCabe *et al.* (1988) *Biotechnology* 6:923-926); aerosol beam transformation (U.S. Published Application No.
30 20010026941; U.S. Patent No. 4,945,050; International Publication No. WO 91/00915; U.S. Published Application No. 2002015066); and *Lec1* transformation (WO 00/28058). Also see Weissinger *et al.* (1988) *Ann. Rev. Genet.* 22:421-477; Sanford *et al.* (1987) *Particulate Science and Technology* 5:27-37; Christou *et al.*

- (1988) *Plant Physiol.* 87:671-674; McCabe *et al.* (1988) *Bio/Technology* 6:923-926; Finer and McMullen (1991) *In Vitro Cell Dev. Biol.* 27P:175-182; Singh *et al.* (1998) *Theor. Appl. Genet.* 96:319-324 (soybean); Datta *et al.* (1990) *Biotechnology* 8:736-740; Klein *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309; U.S. Patent
 5 No. 5,240,855; U.S. Patent Nos. 5,322,783 and 5,324,646; Tomes *et al.* (1995) "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg (Springer-Verlag, Berlin); Klein *et al.* (1988) *Plant Physiol.* 91:440-444; Hooykaas-Van Slogteren *et al.* (1984) *Nature (London)* 311:763-764; U.S. Patent No. 5,736,369;
 10 Bytebier *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:5345-5349 (Liliaceae); De Wet *et al.* (1985) in *The Experimental Manipulation of Ovule Tissues*, ed. Chapman *et al.* (Longman, New York), pp. 197-209; Kaeppler *et al.* (1990) *Plant Cell Reports* 9:415-418 and Kaeppler *et al.* (1992) *Theor. Appl. Genet.* 84:560-566; D'Halluin *et al.* (1992) *Plant Cell* 4:1495-1505; Li *et al.* (1993) *Plant Cell Reports* 12:250-255 and
 15 Christou and Ford (1995) *Annals of Botany* 75:407-413; Osjoda *et al.* (1996) *Nature Biotechnology* 14:745-750; all of which are herein incorporated by reference.

Following integration of heterologous foreign DNA into plant cells, one then applies a maximum threshold level of appropriate selection in the medium to kill the untransformed cells and separate and proliferate the putatively transformed cells that
 20 survive from this selection treatment by transferring regularly to a fresh medium. By continuous passage and challenge with appropriate selection, one identifies and proliferates the cells that are transformed with the plasmid vector. Then molecular and biochemical methods will be used for confirming the presence of the integrated heterologous gene of interest in the genome of transgenic plant.

25 The cells that have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick *et al.* (1986) *Plant Cell Reports* 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having constitutive expression of the desired phenotypic characteristic identified. Two or
 30 more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved. In this manner, the present invention provides transformed seed (also referred to as "transgenic seed")

having a nucleotide construct of the invention, for example, an expression cassette of the invention, stably incorporated into their genome.

The delta-endotoxin or delta-endotoxin-associated sequences of the invention may be provided in expression cassettes for expression in the plant of interest. The cassette will include 5' and 3' regulatory sequences operably linked to a sequence of the invention. By "operably linked" is intended a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame. The cassette may additionally contain at least one additional gene to be cotransformed into the organism. Alternatively, the additional gene(s) can be provided on multiple expression cassettes.

Such an expression cassette is provided with a plurality of restriction sites for insertion of the delta-endotoxin or delta-endotoxin-associated sequence to be under the transcriptional regulation of the regulatory regions.

The expression cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region (i.e., a promoter), a DNA sequence of the invention, and a transcriptional and translational termination region (i.e., termination region) functional in plants. The promoter may be native or analogous, or foreign or heterologous, to the plant host and/or to the DNA sequence of the invention. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. Where the promoter is "native" or "homologous" to the plant host, it is intended that the promoter is found in the native plant into which the promoter is introduced. Where the promoter is "foreign" or "heterologous" to the DNA sequence of the invention, it is intended that the promoter is not the native or naturally occurring promoter for the operably linked DNA sequence of the invention.

The termination region may be native with the transcriptional initiation region, may be native with the operably-linked DNA sequence of interest, may be native with the plant host, or may be derived from another source (i.e., foreign or heterologous to the promoter, the DNA sequence of interest, the plant host, or any combination thereof). Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions.

See also Guerineau *et al.* (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon *et al.* (1991) *Genes Dev.* 5:141-149; Mogen *et al.* (1990) *Plant Cell* 2:1261-1272; Munroe *et al.* (1990) *Gene* 91:151-158; Ballas *et al.* (1989) *Nucleic Acids Res.* 17:7891-7903; and Joshi *et al.* (1987) *Nucleic Acid Res.* 15:9627-9639.

Where appropriate, the gene(s) may be optimized for increased expression in the transformed host cell. That is, the genes can be synthesized using host cell-preferred codons for improved expression, or may be synthesized using codons at a host-preferred codon usage frequency. See, for example, Campbell and Gowri (1990) *Plant Physiol.* 92:1-11 for a discussion of host-preferred codon usage. Methods are known in the art for synthesizing plant-preferred genes. See, for example, U.S. Patent Nos. 6,320,100; 6,075,185; 5,380,831; and 5,436,391, U.S. Published Application Nos. 20040005600 and 20010003849, and Murray *et al.* (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

In one embodiment, the nucleic acids of interest are targeted to the chloroplast for expression. In this manner, where the nucleic acid of interest is not directly inserted into the chloroplast, the expression cassette will additionally contain a nucleic acid encoding a transit peptide to direct the gene product of interest to the chloroplasts. Such transit peptides are known in the art. See, for example, Von Heijne *et al.* (1991) *Plant Mol. Biol. Rep.* 9:104-126; Clark *et al.* (1989) *J. Biol. Chem.* 264:17544-17550; Della-Cioppa *et al.* (1987) *Plant Physiol.* 84:965-968; Romer *et al.* (1993) *Biochem. Biophys. Res. Commun.* 196:1414-1421; and Shah *et al.* (1986) *Science* 233:478-481.

Methods for transformation of chloroplasts are known in the art. See, for example, Svab *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:8526-8530; Svab and Maliga (1993) *Proc. Natl. Acad. Sci. USA* 90:913-917; Svab and Maliga (1993) *EMBO J.* 12:601-606. The method relies on particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination. Additionally, plastid transformation can be accomplished by transactivation of a silent plastid-borne transgene by tissue-preferred expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:7301-7305.

The nucleic acids of interest to be targeted to the chloroplast may be optimized for expression in the chloroplast to account for differences in codon usage between the plant nucleus and this organelle. In this manner, the nucleic acids of interest may be synthesized using chloroplast-preferred codons. See, for example, U.S. Patent No. 5,380,831, herein incorporated by reference.

Evaluation of Plant Transformation

Following introduction of heterologous foreign DNA into plant cells, the transformation or integration of heterologous gene in the plant genome is confirmed by various methods such as analysis of nucleic acids, proteins and metabolites associated with the integrated gene.

PCR Analysis: PCR analysis is a rapid method to screen transformed cells, tissue or shoots for the presence of incorporated gene at the earlier stage before transplanting into the soil (Sambrook and Russell, 2001). PCR is carried out using oligonucleotide primers specific to the gene of interest or *Agrobacterium* vector background, etc.

Southern Analysis: Plant transformation is confirmed by Southern blot analysis of genomic DNA (Sambrook and Russell, 2001). In general, total DNA is extracted from the transformant, digested with appropriate restriction enzymes, fractionated in an agarose gel and transferred to a nitrocellulose or nylon membrane. The membrane or "blot" then is probed with, for example, radiolabeled ^{32}P target DNA fragment to confirm the integration of introduced gene in the plant genome according to standard techniques (Sambrook and Russell, 2001. *Molecular Cloning: A Laboratory Manual*. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

Northern Analysis: RNA is isolated from specific tissues of transformant, fractionated in a formaldehyde agarose gel, blotted onto a nylon filter according to standard procedures that are routinely used in the art (Sambrook, J., and Russell, D.W. 2001. *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). Expression of RNA encoded by the delta-endotoxin or delta-endotoxin-associated is then tested by hybridizing the filter to a radioactive

probe derived from a delta-endotoxin or delta-endotoxin-associated protein, by methods known in the art (Sambrook and Russell, 2001).

Western blot and Biochemical assays: Western blot and biochemical assays and the like may be carried out on the transgenic plants to confirm the presence of protein encoded by the delta-endotoxin or delta-endotoxin-associated gene by standard procedures (Sambrook, J., and Russell, D.W. 2001. *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) using antibodies that bind to one or more epitopes present on the delta-endotoxin or delta-endotoxin-associated protein.

Pesticidal activity in plants

In another aspect of the invention, one may generate transgenic plants expressing delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity. Methods described above by way of example may be utilized to generate transgenic plants, but the manner in which the transgenic plant cells are generated is not critical to this invention. Methods known or described in the art such as *Agrobacterium*-mediated transformation, aerosol beam, biolistic transformation, and non-particle-mediated methods may be used at the discretion of the experimenter. Plants expressing delta-endotoxin or delta-endotoxin-associated proteins may be isolated by common methods described in the art, for example by transformation of callus, selection of transformed callus, and regeneration of fertile plants from such transgenic callus. In such process, one may use any gene as a selectable marker so long as its expression in plant cells confers ability to identify or select for transformed cells.

A number of markers have been developed for use with plant cells, such as resistance to chloramphenicol, the aminoglycoside G418, hygromycin, or the like. Other genes that encode a product involved in chloroplast metabolism may also be used as selectable markers. For example, genes that provide resistance to plant herbicides such as glyphosate, bromoxynil, or imidazolinone may find particular use. Such genes have been reported (Stalker *et al.* (1985) *J. Biol. Chem.* 263:6310-6314 (bromoxynil resistance nitrilase gene); and Sathasivan *et al.* (1990) *Nucl. Acids Res.* 18:2188 (AHAS imidazolinone resistance gene).

Fertile plants expressing a delta-endotoxin or a delta-endotoxin-associated protein may be tested for pesticidal activity, and the plants showing optimal activity selected for further breeding. Methods are available in the art to assay for pest activity. Generally, the protein is mixed and used in feeding assays. See, for example

5 Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293.

Use in Pesticidal Control

General methods for employing the strains of the invention in pesticide control or in engineering other organisms as pesticidal agents are known in the art. See, for

10 example U.S. Patent No. 5,039,523 and EP 0480762A2.

The *Bacillus* strains of the invention or the microorganisms which have been genetically altered to contain the pesticidal gene and protein may be used for protecting agricultural crops and products from pests. In one aspect of the invention, whole, i.e., unlysed, cells of a toxin (pesticide)-producing organism are treated with

15 reagents that prolong the activity of the toxin produced in the cell when the cell is applied to the environment of target pest(s).

Alternatively, the pesticide is produced by introducing a heterologous gene into a cellular host. Expression of the heterologous gene results, directly or indirectly, in the intracellular production and maintenance of the pesticide. In one aspect of this

20 invention, these cells are then treated under conditions that prolong the activity of the toxin produced in the cell when the cell is applied to the environment of target pest(s). The resulting product retains the toxicity of the toxin. These naturally encapsulated pesticides may then be formulated in accordance with conventional techniques for application to the environment hosting a target pest, e.g., soil, water, and foliage of

25 plants. See, for example EPA 0192319, and the references cited therein.

Alternatively, one may formulate the cells expressing the genes of this invention such as to allow application of the resulting material as a pesticide.

The active ingredients of the present invention are normally applied in the form of compositions and can be applied to the crop area or plant to be treated,

30 simultaneously or in succession, with other compounds. These compounds can be fertilizers, weed killers, cryoprotectants, surfactants, detergents, pesticidal soaps, dormant oils, polymers, and/or time-release or biodegradable carrier formulations that permit long-term dosing of a target area following a single application of the

formulation. They can also be selective herbicides, chemical insecticides, virucides, microbicides, amoebicides, pesticides, fungicides, bacteriocides, nematocides, molluscicides or mixtures of several of these preparations, if desired, together with further agriculturally acceptable carriers, surfactants or application-promoting
5 adjuncts customarily employed in the art of formulation. Suitable carriers and
adjuncts can be solid or liquid and correspond to the substances ordinarily employed
in formulation technology, e.g. natural or regenerated mineral substances, solvents,
dispersants, wetting agents, tackifiers, binders or fertilizers. Likewise the formulations
may be prepared into edible "baits" or fashioned into pest "traps" to permit feeding or
10 ingestion by a target pest of the pesticidal formulation.

Preferred methods of applying an active ingredient of the present invention or
an agrochemical composition of the present invention which contains at least one of
the pesticidal proteins produced by the bacterial strains of the present invention are
leaf application, seed coating and soil application. The number of applications and
15 the rate of application depend on the intensity of infestation by the corresponding
pest.

The composition may be formulated as a powder, dust, pellet, granule, spray,
emulsion, colloid, solution, or such like, and may be preparable by such conventional
means as desiccation, lyophilization, homogenation, extraction, filtration,
20 centrifugation, sedimentation, or concentration of a culture of cells comprising the
polypeptide. In all such compositions that contain at least one such pesticidal
polypeptide, the polypeptide may be present in a concentration of from about 1% to
about 99% by weight.

Lepidopteran or coleopteran pests may be killed or reduced in numbers in a
25 given area by the methods of the invention, or may be prophylactically applied to an
environmental area to prevent infestation by a susceptible pest. Preferably the pest
ingests, or is contacted with, a pesticidally-effective amount of the polypeptide. By
"pesticidally-effective amount" is intended an amount of the pesticide that is able to
bring about death to at least one pest, or to noticeably reduce pest growth, feeding, or
30 normal physiological development. This amount will vary depending on such factors
as, for example, the specific target pests to be controlled, the specific environment,
location, plant, crop, or agricultural site to be treated, the environmental conditions,
and the method, rate, concentration, stability, and quantity of application of the

pesticidally-effective polypeptide composition. The formulations may also vary with respect to climatic conditions, environmental considerations, and/or frequency of application and/or severity of pest infestation.

The pesticide compositions described may be made by formulating either the
5 bacterial cell, crystal and/or spore suspension, or isolated protein component with the desired agriculturally-acceptable carrier. The compositions may be formulated prior to administration in an appropriate means such as lyophilized, freeze-dried, desiccated, or in an aqueous carrier, medium or suitable diluent, such as saline or other buffer. The formulated compositions may be in the form of a dust or granular material, or a
10 suspension in oil (vegetable or mineral), or water or oil/water emulsions, or as a wettable powder, or in combination with any other carrier material suitable for agricultural application. Suitable agricultural carriers can be solid or liquid and are well known in the art. The term "agriculturally-acceptable carrier" covers all adjuvants, inert components, dispersants, surfactants, tackifiers, binders, etc. that are
15 ordinarily used in pesticide formulation technology; these are well known to those skilled in pesticide formulation. The formulations may be mixed with one or more solid or liquid adjuvants and prepared by various means, e.g., by homogeneously mixing, blending and/or grinding the pesticidal composition with suitable adjuvants using conventional formulation techniques. Suitable formulations and application
20 methods are described in U.S. Patent No. 6,468,523, herein incorporated by reference.

"Pest" includes but is not limited to, insects, fungi, bacteria, nematodes, mites, ticks, and the like. Insect pests include insects selected from the orders Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthoptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera,
25 Trichoptera, etc., particularly Coleoptera, Lepidoptera, and Diptera.

Insect pests include insects selected from the orders Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthoptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera, etc., particularly Coleoptera and Lepidoptera. Insect pests of the invention for the major
30 crops include: Maize: *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Helicoverpa zea*, corn earworm; *Spodoptera frugiperda*, fall armyworm; *Diatraea grandiosella*, southwestern corn borer; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Diatraea saccharalis*, sugarcane borer; *Diabrotica virgifera*, western

- corn rootworm; *Diabrotica longicornis barberi*, northern corn rootworm; *Diabrotica undecimpunctata howardi*, southern corn rootworm; *Melanotus* spp., wireworms; *Cyclocephala borealis*, northern masked chafer (white grub); *Cyclocephala immaculata*, southern masked chafer (white grub); *Popillia japonica*, Japanese beetle;
- 5 *Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*, corn leaf aphid; *Anuraphis maidiradicis*, corn root aphid; *Blissus leucopterus leucopterus*, chinch bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus sanguinipes*, migratory grasshopper; *Hylemya platura*, seedcorn maggot; *Agromyza parvicornis*, corn blot leafminer; *Anaphothrips*
- 10 *obscurus*, grass thrips; *Solenopsis milesta*, thief ant; *Tetranychus urticae*, twospotted spider mite; Sorghum: *Chilo partellus*, sorghum borer; *Spodoptera frugiperda*, fall armyworm; *Helicoverpa zea*, corn earworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Feltia subterranea*, granulate cutworm; *Phyllophaga crinita*, white grub; *Eleodes*, *Conoderus*, and *Aeolus* spp., wireworms; *Oulema melanopus*, cereal
- 15 leaf beetle; *Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*, corn leaf aphid; *Sipha flava*, yellow sugarcane aphid; *Blissus leucopterus leucopterus*, chinch bug; *Contarinia sorghicola*, sorghum midge; *Tetranychus cinnabarinus*, carmine spider mite; *Tetranychus urticae*, twospotted spider mite; Wheat: *Pseudaletia unipunctata*, army worm; *Spodoptera frugiperda*,
- 20 fall armyworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Agrotis orthogonia*, western cutworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Oulema melanopus*, cereal leaf beetle; *Hypera punctata*, clover leaf weevil; *Diabrotica undecimpunctata howardi*, southern corn rootworm; Russian wheat aphid; *Schizaphis graminum*, greenbug; *Macrosiphum avenae*, English grain aphid; *Melanoplus*
- 25 *femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Melanoplus sanguinipes*, migratory grasshopper; *Mayetiola destructor*, Hessian fly; *Sitodiplosis mosellana*, wheat midge; *Meromyza americana*, wheat stem maggot; *Hylemya coarctata*, wheat bulb fly; *Frankliniella fusca*, tobacco thrips; *Cephus cinctus*, wheat stem sawfly; *Aceria tulipae*, wheat curl mite; Sunflower:
- 30 *Suleima helianthana*, sunflower bud moth; *Homoeosoma electellum*, sunflower moth; *zygogramma exclamationis*, sunflower beetle; *Bothyrus gibbosus*, carrot beetle; *Neolasioptera murtfeldtiana*, sunflower seed midge; Cotton: *Heliothis virescens*, cotton budworm; *Helicoverpa zea*, cotton bollworm; *Spodoptera exigua*, beet

- armyworm; *Pectinophora gossypiella*, pink bollworm; *Anthonomus grandis*, boll weevil; *Aphis gossypii*, cotton aphid; *Pseudatomoscelis seriatus*, cotton fleahopper; *Trialeurodes abutilonea*, bandedwinged whitefly; *Lygus lineolaris*, tarnished plant bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Thrips tabaci*, onion thrips; *Frankliniella fusca*, tobacco thrips; *Tetranychus cinnabarinus*, carmine spider mite; *Tetranychus urticae*, twospotted spider mite; Rice: *Diatraea saccharalis*, sugarcane borer; *Spodoptera frugiperda*, fall armyworm; *Helicoverpa zea*, corn earworm; *Colaspis brunnea*, grape colaspis; *Lissorhoptrus oryzophilus*, rice water weevil; *Sitophilus oryzae*, rice weevil; *Nephotettix nigropictus*, rice leafhopper; *Blissus leucopterus leucopterus*, chinch bug; *Acrosternum hilare*, green stink bug; Soybean: *Pseudophasia includens*, soybean looper; *Anticarsia gemmatilis*, velvetbean caterpillar; *Plathypena scabra*, green cloverworm; *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Spodoptera exigua*, beet armyworm; *Heliothis virescens*, cotton budworm; *Helicoverpa zea*, cotton bollworm; *Epilachna varivestis*, Mexican bean beetle; *Myzus persicae*, green peach aphid; *Empoasca fabae*, potato leafhopper; *Acrosternum hilare*, green stink bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Hylemya platura*, seedcorn maggot; *Sericothrips variabilis*, soybean thrips; *Thrips tabaci*, onion thrips; *Tetranychus turkestanii*, strawberry spider mite; *Tetranychus urticae*, twospotted spider mite; Barley: *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Schizaphis graminum*, greenbug; *Blissus leucopterus leucopterus*, chinch bug; *Acrosternum hilare*, green stink bug; *Euschistus servus*, brown stink bug; *Delia platura*, seedcorn maggot; *Mayetiola destructor*, Hessian fly; *Petrobia latens*, brown wheat mite; Oil Seed Rape: *Brevicoryne brassicae*, cabbage aphid; *Phyllotreta cruciferae*, Flea beetle; *Mamestra configurata*, Bertha armyworm; *Plutella xylostella*, Diamond-back moth; *Delia* spp., Root maggots.

- Nematodes include parasitic nematodes such as root-knot, cyst, and lesion nematodes, including *Heterodera* spp., *Meloidogyne* spp., and *Globodera* spp.; particularly members of the cyst nematodes, including, but not limited to, *Heterodera glycines* (soybean cyst nematode); *Heterodera schachtii* (beet cyst nematode); *Heterodera avenae* (cereal cyst nematode); and *Globodera rostochiensis* and

Globodera pailida (potato cyst nematodes). Lesion nematodes include *Pratylenchus* spp.

The following examples are offered by way of illustration and not by way of limitation.

5

EXPERIMENTAL

Example 1. Extraction of Plasmid DNA

Plasmid DNA from strains ATX 13026 or ATX 13002 were prepared in the following way. A pure culture of strain ATX13026 or strain ATX13002 was grown in large quantities of rich media. The culture was centrifuged to harvest the cell pellet. The cell pellet was then prepared by treatment with SDS by methods known in the art, resulting in breakage of the cell wall and release of DNA. Proteins and large genomic DNA was then precipitated by a high salt concentration. The plasmid DNA was precipitated by standard ethanol precipitation. The plasmid DNA was separated from any remaining chromosomal DNA by high-speed centrifugation through a cesium chloride gradient. The DNA was visualized in the gradient by UV light and the band of lower density (i.e. the lower band) was extracted using a syringe. This band contained the plasmid DNA from the strain (either ATX 13026 or ATX 13002) The quality of the DNA was checked by visualization on an agarose gel by methods known in the art.

Example 2. Cloning of Genes

The purified plasmid DNA was sheared into 5-10 kb sized fragments and the 5' and 3' single stranded overhangs repaired using T4 DNA polymerase and Klenow fragment in the presence of all four dNTPs, as known in the art. Phosphates were then attached to the 5' ends by treatment with T4 polynucleotide kinase, as known in the art. The repaired DNA fragments were ligated overnight into a standard high copy vector (i.e. pBluescript SK+), suitably prepared to accept the inserts as known in the art (for example by digestion with a restriction enzyme producing blunt ends).

The quality of the library was analyzed by digesting a subset of clones with a restriction enzyme known to have a cleavage site flanking the cloning site. A high percentage of clones were determined to contain inserts, with an average insert size of 5-6 kb.

Example 3. High Throughput Sequencing of Library Plates

The libraries prepared by the methods above were plated onto rich media containing the appropriate antibiotic to maintain the plasmids clones, and colonies
5 were individually picked into 96-well blocks containing 2 mls of media containing the appropriate antibiotic. These blocks were grown overnight at 37°C at a shaking speed of 350 rpm. The blocks were centrifuged to harvest the cells to the bottom of the block. Plasmid DNA was isolated from these cultures by standard alkaline lysis prep in a high throughput format.

10 The end sequences of clones from this library were determined for a large number of clones from each block in the following way: The DNA sequence of each clone chosen for analysis was determined using the fluorescent dye terminator sequencing technique (Applied Biosystems) and standard primers flanking each side of the cloning site. Once the reactions had been carried out in the thermocycler, the
15 DNA was precipitated using standard ethanol precipitation. The DNA was resuspended in water and loaded onto a capillary sequencing machine. Each library plate of DNA was sequenced from either end of the cloning site, yielding two reads per plate over each insert.

20 Example 4. Assembly and Screening of Sequencing Data

DNA sequences obtained were compiled into an assembly project and aligned together to form contigs. This can be done efficiently using a computer program, such as Vector NTi, or alternatively by using the Pred/Phrap suite of DNA alignment and analysis programs. These contigs, along with any individual read that may not have
25 been added to a contig, were compared to a compiled database of all classes of known pesticidal genes. Contigs or individual reads identified as having identity to a known endotoxin or pesticidal gene were analyzed further. Among the sequences obtained, clones pAX004, pAX006, pAX007, pAX008, pAX009, and pAX014 contained DNA identified as having homology to known endotoxin genes. Therefore, these clones
30 were selected for further sequencing.

Example 5. Sequencing and Identification of Delta-Endotoxin Genes

Primers were designed to anneal to sequences with homology to endotoxin genes, in a manner such that DNA sequences generated from such primers would overlap existing DNA sequence of the clone(s). This process, known as "oligo walking," is well known in the art. This process was utilized to determine the entire DNA sequence of the region exhibiting homology to a known endotoxin gene. In the case of the clones mentioned above, this process was used to determine the DNA sequence of the entire clone, resulting in a single nucleotide sequence for each gene. The completed DNA sequence was then placed back into the original large assembly for further validation. This allowed incorporation of more DNA sequence reads into the contig, resulting in multiple reads of coverage over the entire region.

Analysis of the DNA sequence of each region with homology to a known endotoxin gene identified an open reading frame with homology to a known delta-endotoxin gene. The open reading frame identified from pAX004 is designated as AXMI-004. The open reading frame identified from pAX006 is designated AXMI-006. The open reading frame identified from pAX007 is designated AXMI-007. The open reading frame identified from pAX008 is designated AXMI-008. The open reading frame identified from pAX009 is designated AXMI-009. The open reading frame identified from pAX014 is designated AXMI-014. The DNA sequence of AXMI-004 is provided as SEQ ID NOS:1 and 2, and the amino acid sequence of the predicted AMXI-004 protein is provided as SEQ ID NO:3. An alternate start site for AXMI-004 at nucleotide 385 of SEQ ID NO:1 generates the amino acid sequence provided as SEQ ID NO:5. The DNA sequence of AXMI-006 is provided as SEQ ID NO:6, and the amino acid sequence of the predicted AMXI-006 protein is provided in SEQ ID NO:7. The DNA sequence of AXMI-007 is provided as SEQ ID NO:8, and the amino acid sequence of the predicted AMXI-007 protein is provided in SEQ ID NO:9. An alternate start site for AXMI-007 at nucleotide 151 of SEQ ID NO:8 generates the amino acid sequence provided as SEQ ID NO:11. The DNA sequence of AXMI-008 is provided as SEQ ID NOS:12 and 13, and the amino acid sequence of the predicted AMXI-008 protein is provided in SEQ ID NO:14. An alternate start site for AXMI-008 at nucleotide 177 of SEQ ID NO:12 generates the amino acid sequence provided as SEQ ID NO:16. Further analysis identified an open reading frame immediately 3' to the end of the AXMI-008 open reading frame. This predicted

amino acid sequence of this orf, referred to herein as AXMI-008orf2, is provided in SEQ ID NO:18. The DNA sequence of AXMI-009 is provided as SEQ ID NO:19, and the amino acid sequence of the predicted AMXI-009 protein is provided in SEQ ID NO:20. An alternate start site for AXMI-009 at nucleotide 34 of SEQ ID NO:19
 5 generates the amino acid sequence provided as SEQ ID NO:22. Another alternate start site for AXMI-009 at nucleotide 64 of SEQ ID NO:19 generates the amino acid sequence provided as SEQ ID NO:24. The DNA sequence of AXMI-014 is provided as SEQ ID NOS:25 and 26, and the amino acid sequence of the predicted AMXI-008 protein is provided as SEQ ID NO:27. An alternate start site for AXMI-014 at
 10 nucleotide 136 of SEQ ID NO:25 generates the amino acid sequence provided as SEQ ID NO:29.

Example 6. Homology of Isolated Genes to Known Endotoxin Genes

Searches of DNA and protein databases with the DNA sequences and amino
 15 acid sequences of the present invention reveal that these sequences are homologous to known endotoxins.

AXMI-004

Figure 1 shows an alignment of AXMI-004 with several endotoxins. Blast
 20 searches identify cry1Ca as having the strongest block of homology, with an overall sequence identity in the toxic domain of 43% (see Table 1).

Table 1. Amino Acid Identity of AXMI-004 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-004	Percent Amino Acid Identity in Toxic Domains
cry1Ac*	17%	30%
cry1Ca*	24%	43%
cry2Aa	12%	12%
cry3Aa	33%	33%
cry1Ia	35%	37%
cry7Aa	19%	31%

AXMI-006

Figure 2 shows an alignment of AXMI-006 with several endotoxins. Blast searches identify cry4Aa as having the strongest block of homology, though alignment of AMXI-006 protein (SEQ ID NO:7) to a large set of endotoxin proteins shows that the most homologous protein is cry10Aa. The overall amino acid identity of cry10Aa to AXMI-006 is 25% (see Table 2). Inspection of the amino acid sequence of AXMI-006 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid identity present solely in the toxin domains (see Table 2, column three). This 'trimmed' alignment is shown in Figure 2.

Table 2. Amino Acid Identity of AXMI-006 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-006	Percent Amino Acid Identity of truncated Toxins to AXMI-006
<i>cry1Aa</i>	11%	17%
<i>cry1Ac</i>	12%	19%
<i>cry1Ia</i>	20%	19%
<i>cry3Aa</i>	20%	19%
<i>cry3Bb</i>	22%	21%
<i>cry4Aa</i>	16%	26%
<i>cry6Aa</i>	5%	4%
<i>cry7Aa</i>	12%	19%
<i>cry8Aa</i>	13%	21%
<i>cry10Aa</i>	25%	25%
<i>cry16Aa</i>	23%	23%
<i>cry19Ba</i>	24%	24%
<i>cry24Aa</i>	19%	20%

15 AXMI-007

Blast searches identify *cry4Aa* as having the strongest block of homology to AXMI-007, though alignment of AMXI-007 protein (SEQ ID NO:9) to a large set of endotoxin proteins shows that the most homologous protein is *cry10Aa*. The overall

amino acid identity of *cry10Aa* to AXMI-007 is 25% (see Table 3). Inspection of the amino acid sequence of AXMI-007 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid

5 identify present solely in the toxin domains (see Table 3, column three). This 'trimmed' alignment is shown in Figure 3.

Table 3. Amino Acid Identity of AXMI-007 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-007	Percent Amino Acid Identity of truncated Toxins to AXMI-007
<i>cry1Aa</i>	11%	17%
<i>cry1Ac</i>	12%	20%
<i>cry1Ia</i>	19%	18%
<i>cry3Aa</i>	19%	19%
<i>cry3Bb</i>	21%	21%
<i>cry4Aa</i>	17%	27%
<i>cry6Aa</i>	5%	4%
<i>cry7Aa</i>	13%	19%
<i>cry8Aa</i>	13%	20%
<i>cry10Aa</i>	25%	25%
<i>cry16Aa</i>	24%	24%
<i>cry19Ba</i>	25%	25%
<i>cry24Aa</i>	19%	19%

10 AXMI-008

Blast searches identify *cry40Aa* as having the strongest block of homology to AXMI-008, and alignment of AMXI-008 protein (SEQ ID NO:14) to a large set of endotoxin proteins shows that the most homologous protein is *cry40Aa*. The overall amino acid identity of *cry40Aa* to AXMI-008 is 66% (see Table 4). Inspection of the

15 amino acid sequence of AXMI-008 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid

identify present solely in the toxin domains (see Table 4, column three). This 'trimmed' alignment is shown in Figure 4.

Table 4. Amino Acid Identity of AXMI-008 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-008	Percent Amino Acid Identity of truncated Toxins to AXMI-008
<i>cry1Aa</i>	11%	20%
<i>cry1Ac</i>	11%	20%
<i>cry1Ia</i>	22%	22%
<i>cry2A</i>	10%	10%
<i>cry3Aa</i>	21%	21%
<i>cry3Bb</i>	21%	21%
<i>cry4Aa</i>	13%	21%
<i>cry4Ba</i>	13%	20%
<i>cry6Aa</i>	5%	5%
<i>cry7Aa</i>	12%	20%
<i>cry8Aa</i>	13%	22%
<i>cry10Aa</i>	20%	20%
<i>cry16Aa</i>	22%	22%
<i>cry19Ba</i>	21%	22%
<i>cry24Aa</i>	26%	26%
<i>cry25Aa</i>	23%	23%
<i>cry39Aa</i>	25%	25%
<i>cry40Aa</i>	66%	66%

5

The open reading frame immediately downstream (3') to the AXMI-008 coding region has homology to known endotoxin-related proteins. Blast searches identify *crybun3orf2* (the downstream orf of *cry40Aa*) as having the strongest block of homology. Several other orf-2 like proteins are present in databases, and an alignment of AMXI-008-orf2 protein (SEQ ID NO:18) to a set of these proteins is shown in Figure 5. These proteins also share homology to the C-terminal non-toxic

10

domain of *cry4Aa* and *cry4Ba*. The overall amino acid identity of AXMI-8-orf2 to *cry40Aaorf2* is 86% (see Table 5).

Table 5. Amino acid identity of AXMI-008-orf2 to related proteins

Protein	Percent amino acid identity to AXMI-008-orf2
<i>crybun3orf2</i> (<i>cry40Aa orf2</i>)	86%
<i>crybun2orf2</i> (<i>cry39Aa orf2</i>)	85%
<i>cry19Aorf2</i>	62%
C-terminus <i>cry4Aa</i>	53%
C-terminus <i>cry4Ba</i>	54%

5

AXMI-009

Blast searches identify *cryBAa* as having the strongest block of homology to AXMI-009, and alignment of AMXI-009 protein (SEQ ID NO:20) to a large set of endotoxin proteins shows that the most homologous proteins are *cry3Ba* and *cry16Aa*.

- 10 The overall amino acid identity of *cry3Ba* and *cry16Aa* to AXMI-009 is 26% (see Table 6). Inspection of the amino acid sequence of AXMI-009 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid identify present solely in the toxin domains (see Table 6,
- 15 column three). This 'trimmed' alignment is shown in Figure 6.

Table 6. Amino Acid Identity of AXMI-009 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-009	Percent Amino Acid Identity of truncated Toxins to AXMI-009
<i>cry1Aa</i>	12%	20%
<i>cry1Ac</i>	13%	23%
<i>cry1Ca</i>	13%	24
<i>cry1Ia</i>	24%	26%
<i>cry3Aa</i>	24%	25%
<i>cry3Ba</i>	26%	27%
<i>cry3Bb</i>	25%	27%
<i>cry4Aa</i>	13%	24%
<i>cry6Aa</i>	7%	5%
<i>cry7Aa</i>	15%	25%
<i>cry8Aa</i>	17%	28%%
<i>cry10Aa</i>	24%	24%
<i>cry16Aa</i>	26%	26%
<i>cry19Ba</i>	24%	25%
<i>cry24Aa</i>	25%	27%
<i>cry25Aa</i>	23%	23%
<i>cry40Aa</i>	19%	24%

AXMI-014

Blast searches identify *cry40Aa* as having the strongest block of homology to AXMI-014, and alignment of AMXI-0014 protein (SEQ ID NO:27) to a large set of endotoxin proteins shows that the most homologous protein is *cry40Aa*. The overall amino acid identity of *cry40Aa* to AXMI-014 is 55% (see Table 7). Inspection of the amino acid sequence of AXMI-014 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid identify present solely in the toxin domains (see Table 7, column three). This 'trimmed' alignment is shown in Figure 7.

Table 7. Amino Acid Identity of AXMI-014 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-014	Percent Amino Acid Identity of truncated Toxins to AXMI-014
<i>cry1Aa</i>	12%	21%
<i>cry1Ac</i>	12%	22%
<i>cry1Ia</i>	20%	21%
<i>cry2A</i>	12%	12%
<i>cry3Aa</i>	20%	20%
<i>cry3Bb</i>	22%	22%
<i>cry4Aa</i>	12%	19%
<i>cry4Ba</i>	11%	19%
<i>cry6Aa</i>	6%	6%
<i>cry7Aa</i>	13%	21%
<i>cry8Aa</i>	14%	22%
<i>cry10Aa</i>	22%	22%
<i>cry16Aa</i>	24%	24%
<i>cry19Ba</i>	24%	24%
<i>cry24Aa</i>	29%	29%
<i>cry25Aa</i>	23%	23%
<i>cry39Aa</i>	22%	22%
<i>cry40Aa</i>	55%	55%

Example 7. Homology between AXMI-006 and AXMI-007

5 Comparison of the amino acid sequences of AXMI-007 with AXMI-006 shows that the two toxins share significant amino acid homology. Alignment of the amino acid sequence of AXMI-006 (SEQ ID NO:7) and AXMI-007 (SEQ ID NO:9) show the proteins to be 85 % identical at the amino acid level. Thus AXMI-006 and AXMI-007 constitute a new class of related endotoxins.

10

Example 8. Assays for Pesticidal Activity

The ability of a pesticidal protein to act as a pesticide upon a pest is often assessed in a number of ways. One way well known in the art is to perform a feeding assay. In such a feeding assay, one exposes the pest to a sample containing either compounds to be tested, or control samples. Often this is performed by placing the material to be tested, or a suitable dilution of such material, onto a material that the pest will ingest, such as an artificial diet. The material to be tested may be composed of a liquid, solid, or slurry. The material to be tested may be placed upon the surface and then allowed to dry. Alternatively, the material to be tested may be mixed with a molten artificial diet, then dispensed into the assay chamber. The assay chamber may be, for example, a cup, a dish, or a well of a microtiter plate.

Assays for sucking pests (for example aphids) may involve separating the test material from the insect by a partition, ideally a portion that can be pierced by the sucking mouthparts of the sucking insect, to allow ingestion of the test material. Often the test material is mixed with a feeding stimulant, such as sucrose, to promote ingestion of the test compound.

Other types of assays can include microinjection of the test material into the mouth, or gut of the pest, as well as development of transgenic plants, followed by test of the ability of the pest to feed upon the transgenic plant. Plant testing may involve isolation of the plant parts normally consumed, for example, small cages attached to a leaf, or isolation of entire plants in cages containing insects.

Other methods and approaches to assay pests are known in the art, and can be found, for example in Robertson, J. L. & H. K. Preisler. 1992. *Pesticide bioassays with arthropods*. CRC, Boca Raton, FL. Alternatively, assays are commonly described in the journals "Arthropod Management Tests" and "Journal of Economic Entomology" or by discussion with members of the Entomological Society of America (ESA).

Example 9. Cloning of AXMI-006 for Protein Expression

AXMI-006 was cloned into a vector for *E. coli* expression as follows. pAX480 contains the kanamycin resistance gene for selection of transformants, and the *tac* promoter which is inducible by IPTG for regulated protein expression. pAX480 was modified by inserting a DNA segment encoding a 6xHis-tag region

immediately upstream of the insert cloning region, such that resulting clones contain a 6xHis-tag at the N-terminus of the expressed protein. Methods for expressing proteins with 6xHis-tag fusions, and their use for purification and analysis of protein expression are well known in the art.

- 5 The coding sequence for AXMI-006 was PCR-amplified using *PfuUltra*TM High-Fidelity DNA Polymerase (Stratagene). Oligonucleotide primers were designed such that the resulting PCR product contained desired restriction sites near each end, to facilitate cloning. The resulting PCR product (approximately 2.2 kb) was digested with the appropriate restriction enzyme, and subcloned into the modified pAX480.
- 10 Insert-containing clones were identified by restriction analysis. The resulting clone, pAX906, contained the AXMI-006 open reading frame fused to the six his tag, such that transcription and translation resulted in production of a 'fusion protein' with a stretch of six histidines. The DNA sequence of pAX906 was confirmed by DNA sequence analysis and subsequently transformed into chemically competent *E. coli*
- 15 BL21, as described by the manufacturer (Stratagene, La Jolla, CA).

A single colony of pAX906 in BL21 was inoculated into LB media supplemented with kanamycin and grown for several hours at 37°C with vigorous agitation. These cultures were grown to an OD₆₀₀ ranging from 0.6-0.8; then protein production was induced by addition of 0.1 mM IPTG. Cultures were grown under

20 inducing conditions for 3 hours, and then the cells were pelleted by centrifugation and resuspended in PBS. Cells were sonicated using a Misonix Sonicator 3000 for a total of 30 seconds using 10-second sonication intervals and incubation on ice for one minute.

25 Example 10. Bioassay of AXMI-006 Activity on *Heliothis virescens* and *Spodoptera frugiperda*

Bioassays of sonicated pAX906 cultures were performed using artificial diet (Multiple Species Diet, Southland Products, Lake Village, Arkansas). Bioassays were carried out by applying sonicated pAX906 cells, or cells of the *E. coli* strain as a

30 control, to the diet surface and allowing the diet surface to dry. Bioassays were performed in 24-well tissue culture plates. The bioassays were held in the dark at 25°C and 65% relative humidity. Trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston, MA). Results were recorded at 5 days.

Table 8. Bioassay of AXMI-006 on *Spodoptera frugiperda*

Sample	Bioassay Result
AXMI-006	Stunting
Negative control	No Stunting

Table 9. Bioassay of AXMI-006 on *Heliothis virescens*

Sample	Bioassay Result
AXMI-006	Stunting
Negative Control	No Stunting

5

Stunting is defined reduced insect size, and severally reduced larval feeding. Stunted insects may also demonstrate avoidance of the treated diet compared to the untreated diet.

10. Example 11. Pesticidal Activity of AXMI-008, AXMI-009, and AXMI-014 on *Trichoplusia ni* (Cabbage Looper)

Escherichia coli strains containing either pAX008, pAX009 or pAX-014, as well as a culture of untransformed *Escherichia coli* were grown in 2 ml of LB Broth (Luria-Bertani Broth, Becton Dickinson & Company, Sparks, Md.) for 24 hours at 37°
 15 C with agitation at 250 rpm. Plasmid-containing strains were grown in LB containing the appropriate antibiotic to select for maintenance of the plasmid in *E. coli*.

Bioassays were performed using artificial diet (Multiple Species Diet, Southland Products, Lake Village, Arkansas) in 24 well tissue culture plates.
 20 Bioassays were carried out by applying the *Escherichia coli* culture containing pAX-014 to the diet surface and allowing the diet surface to dry. The strains were applied as whole cultures to the diet at a concentration of 40 µl of culture per well. The bioassays were held in the dark at 25° C and 65% relative humidity. Trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston, MA). Results
 25 were recorded at 5 days.

Table 10. Pesticidal Activity on *T. ni*

<u>Sample</u>	<u># Dead/ Total</u>	<u>% Mortality</u>
AXMI-014	13/13	100%
AXMI-008	6/6	100%
AXMI-009	17/17	100%
Negative Control	0/13	0%

Example 12. Expression of Delta-Endotoxin Genes in *Bacillus*

5 AXMI-004, AXMI-006, AXMI-007, AXMI-008, and AXMI-009 were amplified by PCR from the clones from Example 4, and cloned into the *Bacillus* Expression vector pAX916 by methods well known in the art. For AXMI-004 the resulting clone was designated pAX920. For AXMI-006 the resulting clone was designated pAX921. For AXMI-007 the resulting clone was designated pAX919. For
 10 AXMI-008 the resulting clone was designated pAX922. For AXMI-009 the resulting clone was designated pAX917. The resulting clones expressed the relevant protein when transformed into cells of a *cry(-)* *Bacillus thuringiensis* strain. The *Bacillus* strains containing delta-endotoxin genes and expressing the delta-endotoxin proteins may be cultured on a variety of conventional growth media. A *Bacillus* strain
 15 containing the desired gene was grown in CYS media (10 g/l Bacto-casitone; 3 g/l yeast extract; 6 g/l KH₂PO₄; 14 g/l K₂HPO₄; 0.5 mM MgSO₄; 0.05 mM MnCl₂; 0.05 mM FeSO₄), until sporulation was evident by microscopic examination. Samples were prepared, and delta-endotoxin proteins were tested for insecticidal activity in bioassays against important insect pests.

20

Methods

To prepare CYS media: 10 g/l Bacto-casitone; 3 g/l yeast extract; 6 g/l KH₂PO₄; 14 g/l K₂HPO₄; 0.5 mM MgSO₄; 0.05 mM MnCl₂; 0.05 mM FeSO₄. The CYS mix should be pH 7, if adjustment is necessary. NaOH or HCl are preferred.
 25 The media is then autoclaved and 100 ml of 10X filtered glucose is added after autoclaving. If the resultant solution is cloudy it can be stirred at room temperature to clear.

Example 13. N-terminal Amino Acid Sequence of AXMI-004 Expressed in *Bacillus*

Analysis of AXMI-004 expressed in *Bacillus* suggested that the protein product detected in these cultures may be reduced in size relative to the full-length AXMI-004 protein. Since many endotoxin proteins are cleaved at the N-terminus after expression in *Bacillus*, we determined the N-terminus of the AXMI-004 protein resulting from *Bacillus* expression. Protein samples from AXMI-004 were separated on PAGE gels, and the protein transferred to PVDF membrane by methods known in the art. The protein band corresponding to AXMI-004 was excised. The N-terminal amino acid sequence of this protein was determined by serial Edman degradation as known in the art. The sequence obtained was as follows:

ERFDKNDAL

Comparison of this amino acid sequence with the sequence of the full length AXMI-004 (SEQ ID NO:3) demonstrates that this amino sequence results from internal cleavage of the AXMI-004 after expression in *Bacillus*, resulting in a protein with an N-terminus corresponding to amino acid 28 of SEQ ID NO:3 (disclosed as SEQ ID NO:5).

Example 14. Bioassay of AXMI-004 on Insect Pests

Insecticidal activity of AXMI-004 was established utilizing accepted bioassay procedures using a sporulated *Bacillus* cell culture lysate expressing AXMI-004. The *Bacillus* culture was grown in 50 ml CYS media for both standard bioassay and LC₅₀ bioassays. The cultures were then grown for 2 to 3 days at 30°C, 250 rpm until the cells were sporulated. Sporulation was determined by examining microscopically for the presence of spores. AXMI-004 protein samples were prepared by centrifugation of the sporulated cultures at 12,000 x g for 10 min. The pellet was collected and resuspended in 4 ml 20 mM Tris-HCl, pH 8.0. The suspension was sonicated for 20 seconds (at top power using a micro probe) while placing the tube on ice. The protein concentration of the sample was determined by electrophoresis on an SDS 4-20% gradient acrylamide gel along with a known quantity of bovine serum albumin (BSA) (Figure 8). The concentration of AXMI-004 was determined to be 0.4 µg/ul.

AXMI-004 insecticidal activity was tested using a surface treatment bioassay with artificial diet (Multiple Species diet, Southland Products, Lake Village, Arkansas) prepared as known in the art. Bioassays were carried out by applying the *Bacillus* culture expressing AXMI-004 to the diet surface and allowing the surface to air-dry. Standard bioassays utilized five eggs per well and LC₅₀ bioassays utilized ten neonate insect larvae per well. The eggs or larvae were applied using a fine tip paintbrush. Standard surface bioassays were carried out in 24 well tissue culture plates. 40ul of each sample was applied to each well. Since each well has a surface area of 2 cm² (plate source), a 40 µl cell lysate sample contained approximately 0.4 µg/ul AXMI-004. Bioassays where the LC₅₀ was determined were done in 48 well tissue culture plates, each well representing a surface area of 1 cm² (source) using approximately 20ul of 0.4 µg/ul AXMI-004 per well. The final amount of AXMI-004 protein in each bioassay was approximately 8 µg/cm². Bioassay trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston MA). Control samples included media only samples, and wells that were not treated with samples. Bioassays were then held for five days in the dark at 25° C and 65% relative humidity and results recorded.

Table 11. Insecticidal Activity of AXMI-004

<u>Insect (Latin Name)</u>	<u>Common Name</u>	<u>Activity of AXMI-004</u>
<i>Ostrinia nubilalis</i>	European Corn Borer	100% mortality
<i>Agrotis ipsilon</i>	Black Cutworm	Stunted
<i>Heliothis zea</i>	Corn Earworm	Stunted
<i>Spodoptera frugiperda</i>	Fall Armyworm	Stunted
<i>Heliothis virescens</i>	Tobacco Budworm	100% mortality
<i>Pectinophora gossypiella</i>	Pink Bollworm	75% mortality
<i>Manduca sexta</i>	Tobacco Hornworm	100% mortality
<i>Trichoplusia ni</i>	Cabbage Looper	100% mortality

20

AXMI-004 showed strong insecticidal activity (100% mortality) against *Ostrinia nubilalis* and *Heliothis virescens*. AXMI-004 also showed insecticidal activity of 50-75% mortality against *Pectinophora gossypiella*. A concentration of 43 $\mu\text{g}/\text{cm}^2$ AXMI-004 gave 70% mortality against *Pectinophora gossypiella*. AXMI-004 severely stunted the growth of *Agrotis ipsilon*, *Heliothis zea*, and *Spodoptera frugiperda*.

Example 15. Quantitation of AXMI-004 Insecticidal Activity against *Heliothis virescens* and *Ostrinia nubilalis*

The LC_{50} of AXMI-004 protein on *Ostrinia nubilalis* and *Heliothis virescens* larvae were determined by testing a range of AXMI-004 protein concentrations in insect bioassays, and applying these protein samples to the surface of insect diet. Mortality was recorded at each protein concentration and analyzed using a Probit analysis program. Results were significant at the 95% confidence interval. Since assays were performed by surface contamination, LC_{50} s were determined assuming that the entire protein sample remained at the surface during the assay, with little diffusion below the level ingested by the insects. Thus, the values determined may somewhat underestimate the toxicity of the AXMI-004 protein on the tested insects.

Table 12. LC_{50} of AXMI-004 on *Ostrinia nubilalis*

<u>AXMI-004 ($\mu\text{g}/\text{ml}$)</u>	<u># dead/total</u>	<u>% Mortality</u>
1000	40/46	86.9
500	28/45	62.2
250	16/43	32.7
125	12/38	31.6

$\text{LC}_{50} = 297 \text{ ng}/\text{cm}^2$; 95% CI = 218-384.

Table 13. LC₅₀ of AXMI-004 on *Heliothis virescens*

<u>AXMI-004 (µg/ml)</u>	<u># dead/total</u>	<u>% Mortality</u>
8000	35/47	74.5
4000	26/44	59.1
2000	18/42	42.9
1000	6/27	22.2
500	4/36	11.1
250	2/37	5.4

$$LC_{50} = 2874 \text{ ng/cm}^2; 95\% \text{ CI} = 2189-3933$$

5 Example 16. Quantitation of AXMI-004, AXMI-006, AXMI-007, and AXMI-009
Insecticidal Activity against *Lygus lineolaris*

Bacterial lysates were prepared by growing the *Bacillus* in 50 ml of CYS media for 60 hours. The *Bacillus* culture was then centrifuged at 12,000 rpm for ten minutes and the supernatant discarded. The pellet was resuspended in 5 ml of 20 mM
 10 Tris HCl at pH 8.

Bioassays were performed by cutting both the tip and the cap off an Eppendorf tube to form a feeding chamber. The insecticidal protein or control was presented to the insect in a solution that was poured into the cap and covered with parafilm (Pechiney Plastic Packaging, Chicago IL) that the insect could pierce upon feeding.
 15 The Eppendorf tube was placed back on the cap top down and 1st or 2nd instar *Lygus* nymphs were placed into the Eppendorf chamber with a fine tip brush. The cut Eppendorf tube tip was sealed with parafilm creating an assay chamber. The resultant assay chamber was incubated at ambient temperature cap side down. Insecticidal proteins were tested in a solution of 15% glucose at a concentration of 6.6 µg/ml.

20

Table 14. Insecticidal Activity on *Lygus lineolaris*

Protein	No. Dead/Total	% Mortality
AXMI-004	2/4	50%
AXMI-006	1/6	16.7%
AXMI-007	3/6	50%
AXMI-009	2/4	50%
Control	0/9	0%

Example 17. Bioassay of AXMI-008 on *Tenebrio molitor*

5 Samples of *Bacillus* cultures expressing AXMI-008 were prepared and tested for pesticidal activity on *Tenebrio molitor*. When pAX 922 is prepared as an insoluble fraction at pH 4.0 it showed activity against commonly called the yellow mealworm.

 Samples of AXMI-008 were prepared from a culture of a *Bacillus* strain containing pAX 922. The bioassay sample was prepared by growing a culture in CYS
 10 media for 4 days, until sporulation. The sample was centrifuged at 10,000 rpm for 10 minutes and the supernatant discarded. The pellet was washed in 20mM Tris pH 8 and spun at 10,000 rpm for 10 minutes. The supernatant was discarded and the pellet resuspended in 3 mls of 50 mM Sodium Citrate and 25 mM Sodium Chloride with 2mM DTT at pH 4. The sample was incubated at 37° C for 1 hour. After incubation
 15 the sample was spun at 13,000 rpm for 10 minutes and the supernatant discarded. The pellet was resuspended in 50 mM Sodium Citrate and 25 mM Sodium Chloride at pH 4.

 Bioassays of samples on *Tenebrio molitor* were performed on an artificial diet (Southern Corn Rootworm Diet, Bioserv, Frenchtown, NJ, #F9757B) in 24 well tissue
 20 culture plates. The sample was applied as a surface treatment with a concentration of Axmi008 at 8 ug/cm² and allowed to air dry. The insects were applied using a fine tip brush. Bioassay trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston, MA) and incubated without light at 65% relative humidity, 25° C. for seven days and results recorded.

25

Table 15. Pesticidal Activity of AXMI-008 on *T. molitor*

Sample	# Dead/ Total	% Mortality
AXMI-008	3 of 4	75%*

* Remaining *Tenebrio molitor* was stunted. Stunting is observed as reduced larval size and growth, and severely reduced or minimal feeding. The insect may also demonstrate avoidance of the treated diet compared to the untreated diet.

5

Example 18. Bioassay of AXMI-009 Protein on Coleopteran Pests

Bioassays of AXMI-009 protein preparations were performed by pipetting 40 μ l of insoluble fraction onto a 2 cm² diet surface for a final total protein concentration of 8 μ g/cm². *Diabrotica virgifera virgifera* and *Diabrotica undecimpunctata* were tested using Southern Corn Rootworm Diet (Bioserv, Frenchtown, NJ, #F9757B). Bioassays were carried out by applying the *Bacillus* culture expressing AXMI-009 to the diet surface and allowing the diet surface to dry. Bioassays were performed in 24 well tissue culture plates. Standard bioassays utilized 25 eggs per well. The eggs were applied in a solution containing 0.1% agar and 30 ug/ml nystatin. Trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston, MA) and the lids placed back on the trays. Bioassays were incubated without light at 65% Relative Humidity (RH), 25° C for seven days. Activity was seen with the insoluble fraction for both *Diabrotica virgifera virgifera* and *Diabrotica undecimpunctata*. Controls were a media only, buffer of 1 mM Tris at pH 10.5, and the *Bacillus* expression vector pAX916.

20

Table 16. Western Corn Rootworm (*Diabrotica virgifera virgifera*)

	# Dead/Total	% Mortality
AXMI-009 insoluble fraction	38/38	100%
Media only (CYS)	1/25	4%
Buffer	2/24	8.3%
Vector (pAX916)	1/12	8.3%

Table 17. Southern Corn Rootworm (*Diabrotica undecimpunctata*)

	<u># Dead/Total</u>	<u>% Mortality</u>
AXMI-009 insoluble fraction	20/20	100%
Media only (CYS)	0/20	0%
Buffer	0/23	0%
Vector (pAX916)	0/19	0%

Example 19. Vectoring for Plant Expression

The delta-endotoxin coding region DNA is operably connected with appropriate promoter and terminator sequences for expression in plants. Such sequences are well known in the art and may include the rice actin promoter or maize ubiquitin promoter for expression in monocots, the *Arabidopsis* UBQ3 promoter or CaMV 35S promoter for expression in dicots, and the nos or PinII terminators. Techniques for producing and confirming promoter – gene – terminator constructs also are well known in the art.

The plant expression cassettes described above are combined with an appropriate plant selectable marker to aid in the selections of transformed cells and tissues, and ligated into plant transformation vectors. These may include binary vectors from *Agrobacterium*-mediated transformation or simple plasmid vectors for aerosol or biolistic transformation.

Example 20. Transformation of Maize Cells

Maize ears are collected 8-12 days after pollination. Embryos are isolated from the ears, and those embryos 0.8-1.5 mm in size are used for transformation. Embryos are plated scutellum side-up on a suitable incubation media, such as DN62A5S media (3.98 g/L N6 Salts; 1 mL/L (of 1000x Stock) N6 Vitamins; 800 mg/L L-Asparagine; 100 mg/L Myo-inositol; 1.4 g/L L-Proline; 100 mg/L Casaminoacids; 50 g/L sucrose; 1 mL/L (of 1 mg/mL Stock) 2,4-D), and incubated overnight at 25°C in the dark.

The resulting explants are transferred to mesh squares (30-40 per plate), transferred onto osmotic media for 30-45 minutes, then transferred to a beaming plate (see, for example, PCT Publication No. WO/0138514 and U.S. Patent No. 5,240,842).

DNA constructs designed to express the delta-endotoxin in plant cells are accelerated into plant tissue using an aerosol beam accelerator, using conditions

essentially as described in PCT Publication No. WO/0138514. After beaming, embryos are incubated for 30 min on osmotic media, then placed onto incubation media overnight at 25°C in the dark. To avoid unduly damaging beamed explants, they are incubated for at least 24 hours prior to transfer to recovery media. Embryos

5 are then spread onto recovery period media, for 5 days, 25°C in the dark, then transferred to a selection media. Explants are incubated in selection media for up to eight weeks, depending on the nature and characteristics of the particular selection utilized. After the selection period, the resulting callus is transferred to embryo

10 maturation media, until the formation of mature somatic embryos is observed. The resulting mature somatic embryos are then placed under low light, and the process of regeneration is initiated by methods known in the art. The resulting shoots are allowed to root on rooting media, and the resulting plants are transferred to nursery pots and propagated as transgenic plants.

15 *Materials*

DN62A5S Media

Components	per liter	Source
Chu'S N6 Basal Salt Mixture (Prod. No. C 416)	3.98 g/L	Phytotechnology Labs
Chu's N6 Vitamin Solution (Prod. No. C 149)	1 mL/L (of 1000x Stock)	Phytotechnology Labs
L-Asparagine	800 mg/L	Phytotechnology Labs
Myo-inositol	100 mg/L	Sigma
L-Proline	1.4 g/L	Phytotechnology Labs
Casaminoacids	100 mg/L	Fisher Scientific
Sucrose	50 g/L	Phytotechnology Labs
2,4-D (Prod. No. D-7299)	1 mL/L (of 1 mg/mL Stock)	Sigma

Adjust the pH of the solution to pH to 5.8 with 1N KOH/1N KCl, add Gelrite (Sigma) to 3g/L, and autoclave. After cooling to 50°C, add 2 ml/L of a 5 mg/ml stock

20 solution of Silver Nitrate (Phytotechnology Labs). Recipe yields about 20 plates.

Example 21. Transformation into Plant Cells by *Agrobacterium*-Mediated Transformation

Ears are collected 8-12 days after pollination. Embryos are isolated from the
5 ears, and those embryos 0.8-1.5 mm in size are used for transformation. Embryos are
plated scutellum side-up on a suitable incubation media, and incubated overnight at
25°C in the dark. However, it is not necessary *per se* to incubate the embryos
overnight. Embryos are contacted with an *Agrobacterium* strain containing the
appropriate vectors for Ti plasmid mediated transfer for 5-10 min, and then plated
10 onto co-cultivation media for 3 days (25°C in the dark). After co-cultivation, explants
are transferred to recovery period media for five days (at 25°C in the dark). Explants
are incubated in selection media for up to eight weeks, depending on the nature and
characteristics of the particular selection utilized. After the selection period, the
resulting callus is transferred to embryo maturation media, until the formation of
15 mature somatic embryos is observed. The resulting mature somatic embryos are then
placed under low light, and the process of regeneration is initiated as known in the art.
The resulting shoots are allowed to root on rooting media, and the resulting plants are
transferred to nursery pots and propagated as transgenic plants.

20 Conclusions

The delta-endotoxin proteins of the present invention have activity against
numerous pests, as shown in the examples above. AXMI-004 has pesticidal activity
against pests including *Ostrinia nubilalis*, *Agrotis ipsilon*, *Heliothis zea*, *Spodoptera*
frugiperda, *Heliothis virescens*, *Pectinophora gossypiella*, *Manduca Sexta*,
25 *Trichoplusia ni*, and *Lygus lineolaris*. AXMI-006 has pesticidal activity against pests
including *Heliothis virescens*, *Spodoptera frugiperda*, and *Lygus lineolaris*. AXMI-
007 has pesticidal activity against pests including *Lygus lineolaris*. AXMI-008 has
pesticidal activity against pests including *Tenebrio molitor* and *Trichoplusia ni*.
AXMI-009 has pesticidal activity against pests including *Lygus lineolaris*,
30 *Trichoplusia ni*, *Diabrotica virgifera virgifera*, and *Diabrotica undecimpunctata*.
AXMI-014 has pesticidal activity against pests including *Trichoplusia ni*.

All publications and patent applications mentioned in the specification are
indicative of the level of skill of those skilled in the art to which this invention

pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

- 5 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

THAT WHICH IS CLAIMED:

1. An isolated nucleic acid molecule selected from the group consisting of:
 - a) a nucleic acid molecule comprising the nucleotide sequence of
5 SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28;
 - b) a nucleic acid molecule comprising a nucleotide sequence having at least 95% sequence identity to the nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, wherein said nucleotide sequence encodes a polypeptide having pesticidal activity;
 - 10 c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29;
 - d) a nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 95% amino acid sequence identity to the amino acid
15 sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity; and,
 - e) a complement of any of a)-d).
2. An isolated nucleic acid molecule of claim 1, wherein said nucleotide
20 sequence is a synthetic sequence that has been designed for expression in a plant.
3. The nucleic acid molecule of claim 2, wherein said synthetic sequence has an increased GC content.
- 25 4. A vector comprising the nucleic acid molecule of claim 1.
5. The vector of claim 4, further comprising a nucleic acid molecule encoding a heterologous polypeptide.
- 30 6. A host cell that contains the vector of claim 4.
7. The host cell of claim 6 that is a bacterial host cell.

8. The host cell of claim 6 that is a plant cell.
9. A transgenic plant comprising the host cell of claim 8.
- 5 10. The transgenic plant of claim 9, wherein said plant is selected from the group consisting of maize, sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, and oilseed rape.
- 10 11. Transgenic seed of a plant of claim 9.
12. An isolated polypeptide selected from the group consisting of:
- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29;
- b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, wherein said polypeptide has pesticidal activity;
- 15 c) a polypeptide comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity; and,
- 20 d) a polypeptide that is encoded by a nucleotide sequence that is at least 95% identical to the nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28.
- 25 13. The polypeptide of claim 12, further comprising a heterologous amino acid sequence.
14. An antibody that selectively binds to a polypeptide of claim 12.
15. A composition comprising the polypeptide of claim 12.
- 30 16. The composition of claim 15, wherein said composition is selected from the group consisting of a powder, dust, pellet, granule, spray, emulsion, colloid, and solution.

17. The composition of claim 15, wherein said composition is prepared by desiccation, lyophilization, homogenization, extraction, filtration, centrifugation, sedimentation, or concentration of a culture of *Bacillus thuringiensis* cells.

5

18. The composition of claim 15, comprising from about 1% to about 99% by weight of said polypeptide.

19. A method for producing a polypeptide with pesticidal activity, comprising culturing the host cell of claim 6 under conditions in which a nucleic acid molecule encoding the polypeptide is expressed, said polypeptide being selected from the group consisting of:

a) a polypeptide comprising the amino acid of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, wherein said polypeptide has pesticidal activity;

c) a polypeptide comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity; and,

d) a polypeptide that is encoded by a nucleotide sequence that is at least 95% identical to a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28.

20. A method for controlling a lepidopteran or coleopteran pest population comprising contacting said population with a pesticidally-effective amount of a polypeptide of claim 12.

21. A method for killing a lepidopteran or coleopteran pest, comprising contacting said pest with, or feeding to said pest, a pesticidally-effective amount of a polypeptide of claim 12.

22. A plant having stably incorporated into its genome a DNA construct comprising a nucleotide sequence that encodes a protein having pesticidal activity, wherein said nucleotide sequence is selected from the group consisting of:

- a) a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 19, 21, 23, 25, 26, or 28;
 - b) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 19, 21, 23, 25, 26, or 28, wherein said nucleotide sequence encodes a polypeptide having pesticidal activity;
 - c) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22, 24, 27, or 29; and,
 - d) a nucleotide sequence encoding a polypeptide having at least 95% amino acid sequence identity to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity;
- wherein said nucleotide sequence is operably linked to a promoter that drives expression of a coding sequence in a plant cell.

23. The plant of claim 22, wherein said plant further comprises the nucleotide sequence of SEQ ID NO:17.

24. A plant cell having stably incorporated into its genome a DNA construct comprising a nucleotide sequence that encodes a protein having pesticidal activity, wherein said nucleotide sequence is selected from the group consisting of:

- a) a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 19, 21, 23, 25, 26, or 28;
- b) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 19, 21, 23, 25, 26, or 28, wherein said nucleotide sequence encodes a polypeptide having pesticidal activity;
- c) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22, 24, 27, or 29; and,
- d) a nucleotide sequence encoding a polypeptide having at least 95% amino acid sequence identity to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity;

wherein said nucleotide sequence is operably linked to a promoter that drives expression of a coding sequence in a plant cell.

25. The plant cell of claim 24, wherein said plant cell further comprises the
5 nucleotide sequence of SEQ ID NO:17.

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AXHI-004 : -----HSEIKGKPKKSTNRKCLL-----KQINIGGRCHNSKHDYLVKCHDLSANI-NH--ERFDKIDALEYCHSVSEVLAHNP--GGTA : 78
cry1Ac : -----HNNPFIIECIFYNCLSNP-----EVEVLGGERIEFG-----YTPIDISSTITQFLSEFVP--GAGF : 56
cry1Ca : -----HEEN--HONOCIPYVCLSNP-----EEVLDGGERISIG-----NESHDISSITVQFLSNFVP--GGGF : 55
cry2Aa : -----HNNYLSGRITTCDAYNVAHDPPSFEKSLDTQKEUHEUKR-----TDSNYVAPVGTGVSFLKRVQSLI : 69
cry3Aa : MIRKGGRRKPNRSEHDTIKTITENNEVPTNRHVOYPLAETPNPTLEDLNYKEFLRHTADNNTALDSSITKIVQKCHSVGDIQGVGVFFGGA : 95
cry1Ia : -----HNNYLSGRITTCDAYNVAHDPPSFEKSLDTQKEUHEUKR-----TDSNYVAPVGTGVSFLKRVQSLI : 69
cry7Aa : -----HNNYLSGRITTCDAYNVAHDPPSFEKSLDTQKEUHEUKR-----TDSNYVAPVGTGVSFLKRVQSLI : 69
n
AXHI-004 : 100 120 140 160 180
cry1Ac : 100 120 140 160 180
cry1Ca : 100 120 140 160 180
cry2Aa : 100 120 140 160 180
cry3Aa : 100 120 140 160 180
cry1Ia : 100 120 140 160 180
cry7Aa : 100 120 140 160 180
p w f6 E 61 46 n a L 66 S S 6
AXHI-004 : 200 220 240 260 280
cry1Ac : 200 220 240 260 280
cry1Ca : 200 220 240 260 280
cry2Aa : 200 220 240 260 280
cry3Aa : 200 220 240 260 280
cry1Ia : 200 220 240 260 280
cry7Aa : 200 220 240 260 280
6P F 6 26 1L 5 QAAN HL 64D 6 g WG 6 y Y c Y q1 6 w n Rr 6
AXHI-004 : 300 320 340 360 380
cry1Ac : 300 320 340 360 380
cry1Ca : 300 320 340 360 380
cry2Aa : 300 320 340 360 380
cry3Aa : 300 320 340 360 380
cry1Ia : 300 320 340 360 380
cry7Aa : 300 320 340 360 380
L vld a Sp d y Ltr t R phl 6 6 3
AXHI-004 : 400 420 440 460
cry1Ac : 400 420 440 460
cry1Ca : 400 420 440 460
cry2Aa : 400 420 440 460
cry3Aa : 400 420 440 460
cry1Ia : 400 420 440 460
cry7Aa : 400 420 440 460
w g
AXHI-004 : 480 500 520 540 560
cry1Ac : 480 500 520 540 560
cry1Ca : 480 500 520 540 560
cry2Aa : 480 500 520 540 560
cry3Aa : 480 500 520 540 560
cry1Ia : 480 500 520 540 560
cry7Aa : 480 500 520 540 560
ds pp p hrl w 3 n i it F vk v up fctGD 6
AXHI-004 : 580 600 620 640 660
cry1Ac : 580 600 620 640 660
cry1Ca : 580 600 620 640 660
cry2Aa : 580 600 620 640 660
cry3Aa : 580 600 620 640 660
cry1Ia : 580 600 620 640 660
cry7Aa : 580 600 620 640 660
g Y T 1 5
AXHI-004 : 680 700 720
cry1Ac : 680 700 720
cry1Ca : 680 700 720
cry2Aa : 680 700 720
cry3Aa : 680 700 720
cry1Ia : 680 700 720
cry7Aa : 680 700 720
6d 1ef6p

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Fig. 1

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*      *      *      *
20      40      60
exmi006 : -----HQNQNNNNHVEYIDDSHTSPYFPFRNSNDSPYTTNNQNPQONTNKKCDMMCCGNTQYGDNFETPAS : 68
cry1Aa : -----MDNNP-----NINECIPNCLSMDEVEVLGG----- : 26
cry1Ac : -----MDNNP-----NINECIPNCLSMDEVEVLGG----- : 26
cry1Ia : -----MKLKNQDKHQSFSSNAKVD-----KISTDS-----EKQETDIELQMIQHEDCMKHSTYEN----- : 50
cry3Aa1 : MIRKGGKKNPNMNRSEHDTIKITENNE-----VPTNHVOYPLAETDNPPTCDLNYKCFEETADNN-----TE : 63
cry3Ba : MIRKGGKKNPNMNRSEYOTIKVTPSE-----LPTNHNOYPLAEDNPSTLEEANYSKCFEETADNS-----TE : 63
cry4Aa : -----HNPYQDKMEYETIDNASOKKLN-----KSNYTRITPLENSKQLQSTNYKDMNNCCQNNQ-----YGG : 59
cry6Aa : ----- : -
cry7Aa : -----MLNNLDGYEDSNR-----TLNNSLNYPTOKALSPSKNNYQDFSTIREQP----- : 49
cry8Aa : -----NSPNNQMEYEIDDAIPSTS-----VSSDSNRYPFAEDIDALQNNYKDYKRSUGGENPEL-----FG : 58
cry10Aa : -----HNPYQDKMEYEITFNAPSNGFS-----KSNYSTRYPLAKRNQPLKNTYKDMNNVCCDNOQYGN-----AG : 62
cry16Aa : -----HHYQGMMEYDILNASSSDS-----NNSNTYPRYPLAPQDLDQNNYKDMNNVCEGYHIENP-----RE : 61
cry19Ba : -----HNSYQDKMEYEIDAKRNTC-----HNSNCPYKPLADQSNYLRNTHYKDMNNMCEASYAS----- : 58
cry24Aa : -----HNPYQDKMEYEIDESSQNNEN-----MPNRYPPADDENAVHRNGYKDMNNMCEGGSN----- : 52
      ey      n      yp      p      nykd

*      *      *      *
60      100      120      140
exmi006 : ADTIAAVSAGTIIVSGTLLAGHGLTSISGPTGIGATISGTHITVDFPAGEQDKTVTQTFKMGCEITVDFPT : 143
cry1Aa : -----ERIEHGYTPDDISLSLTQFLSEF-----VFGAGFVGLVDIIRUGHFQPSQ-----MDAPVQTEOLINQRE : 89
cry1Ac : -----ERIEHGYTPDDISLSLTQFLSEF-----VFGAGFVGLVDIIRUGHFQPSQ-----MDAPVQTEOLINQRE : 89
cry1Ia : -----VEPFVSASTHQTGICIAKGLGTLG-----VDFAGQVASLSFLLGELDT-KG-----KNQCEITFEHVEEALHOKIS : 117
cry3Aa1 : ALDSSTIKDVHOKGISVVGDLGVVG-----PFGGALVSFTINFLATNPS-----EDPKAFHAEQVEEALHOKIA : 130
cry3Ba : VLDSSVTKDAVGTGISVVGDLGVVG-----VDFAGALTSFVQSFNATLPSD-----ADPKAFHAEQVEEALHOKIE : 131
cry4Aa : DFEFTIDSGLSAYTIIVGTVLTGFG-----FTTFLGLATIGSGTILIPVLFPAQDQSN-TQSDFTITQKNLKKELA : 130
cry6Aa : ----- : -
cry7Aa : -----EALASGNTADNTVSVTGCATLSALG-----VFGASFTINFLKAGLILPENG-----KI-----DOEFTIEEALIDOKIE : 116
cry8Aa : NPETFISSTHQTGICIVGRILGALG-----VDFASQHASFSYFVGLQPSKS-----VDIUGEIERVEEALVQKRE : 127
cry10Aa : NFASSETIVGSAGILIVGTHLCAFA-----ADVLAAGLISGTHLPIHPQGSDDPAN-----VWODLNTGGRFQIEID : 131
cry16Aa : ASVRAGLGKGLGIVSTIVGFFGS-----IILDTEGLFYONSELLPBDTQOYTQODIANHVEDLIDKRT : 128
cry19Ba : S-----GPSQLFKVGGSIYAKILG-----MIFVYGPLLSHNSLFFUPTLEEKNTVDEEDNKYVAMLLKOEIT : 120
cry24Aa : -----ISFSPAAATTSKIVSYIVKTLAKAVASSLADSDKSSLGISKITITENNV-----QVSIVQVHOLITRRIQ : 117
      g lg      p      p      w f e q

*      *      *      *
160      180      200      220
exmi006 : ESRQOLKLTDECFRQIIQ-SNTALDDRKIKRLQAPGLPPSSALQQAALTLLKIRFENVHNDFFREIPGFQLE : 216
cry1Aa : EFARNDALSRDEGLSNLYQ-IVAESFREDEADPTN-----PALREEDRIQENDINSALTATPLAVQN----- : 152
cry1Ac : EFARNDALSRDEGLSNLYQ-IVAESFREDEADPTN-----PALREEDRIQENDINSALTATPLAVQN----- : 152
cry1Ia : TYARKKALDRLGLQDAIA-VVHDSIESOVGRNN-----TRANSVKSQIALLELTVQKLESFAVSG----- : 180
cry3Aa1 : DYAKKALAELOGLOQNNVE-DVYSALSSQORQPVSS-----RNPHSQGRRELISQAESHERNSHPSAISG : 196
cry3Ba : EYAKKALAELOGLOQNNTE-DVYNALSSQKAPVNL-----RSRRSQDRRELISQAESHERNSHPSAVSK----- : 197
cry4Aa : STYISNKKILNRSFNVIS-TYNNHKTIDEMTPN-----PONTQDRTIQQLHYHQRONVLELNVSCPPN : 195
cry6Aa : ----- : -
cry7Aa : EYVKKALAELOGGSAID-KYQKALADILGKODD-----PEALLSWATERIIDSLREFSHPSKVTG----- : 179
cry8Aa : KYVKKALAELOGGSAID-VYQQSLEDLELRND-----ARTRSVSNQIALDLNVSSTHPSFAVSG----- : 190
cry10Aa : KNRIMVLTISIVTPKQOJD-KYQEFFDRQEPARTH-----ANAKAVHDLSTTEPIIDKDDHLKNNAS----- : 194
cry16Aa : EYDEGNVRTIADLQKQD-DYNNHKKQKQKDP-----KSTGNLSTIVTKITAQSDENGARITVNNQESP : 193
cry19Ba : NDTLNRATSMLSGLNESLN-TYNNRALLAKQKQK-----NNFASGELDRSYINDPHILSTRDQSDPSLG----- : 183
cry24Aa : ETILDLGESSLNGVATYMRDYLGADEANNNKSN-----INYOTNVAEAKTVEREPFTRKGYRHS----- : 182
      a      g      y l w      f      p

*      *      *      *
240      260      280      300
exmi006 : -----TVKTLLEPIYQAAMHHLNHLQQAELADEWADIHPSQIEPNAGTSDDYK-LLKENTPKYSNYCANTY : 285
cry1Aa : -----YQVPLLSVYVQAAMHHLNHLSDRDVSVFG-----QRNGFDAATINSRYN-DLTRLIGNYTDYAVROY : 211
cry1Ac : -----YQVPLLSVYVQAAMHHLNHLSDRDVSVFG-----QRNGFDAATINSRYN-DLTRLIGNYTDYAVROY : 211
cry1Ia : -----EEVPLLEPIYQAAMHHLNHLRDASIFG-----KEGGLSSSEISTYNN-RQVERAGDYSDECVKRY : 239
cry3Aa1 : -----VEVPLLEPIYQAAMHHLNHLKDAQITG-----EEGCKEEDHAEFK-RQLKLTQETIDHEVKQY : 255
cry3Ba : -----EEVPLLEPIYQAAMHHLNHLKDAQVFG-----EEGCKESSEDAEYQ-RQLKLTQETIDHEVKQY : 256
cry4Aa : PSDCDYNNLVSSYQAAMHHLNHLNQNVRKREAYLKNN-ROFDHLEPLTAIDNP-VLTKAIEDYNYCVITY : 268
cry6Aa : -----MIDSKITLPRHSLHHTTKNSKKYK-----PGDITNGNQ-----FISKQEWATIGATY : 51
cry7Aa : -----VEPLLEPIYQAAMHHLNHLRDSTLYG-----DKNGFTQNNHTEENY-RQKRLSEYSDHCTQY : 238
cry8Aa : -----HEVLLAVYQAAMHHLNHLRDASIFG-----EEGCTPGLISRYN-RQVQMTAEYSYDQVQY : 249
cry10Aa : -----YRNPILPAYQAAMHHLNHLNAAVYNIULQN-----QGINPSTFNSSNYQCYLKRKIQEYTDYCTQY : 260
cry16Aa : -----GYELLLPYYQAAMHHLNHLRDQITG-----KQUSARANARDNYQ-IQLEKTYEYECIMY : 254
cry19Ba : -----GYELVLLSYQAAMHHLNHLRDQITG-----KELGYPSTDEHYQ-EQKYITEKYSNYCANTY : 243
cry24Aa : -----SQITLLPPIYQAAMHHLNHLRDVNIQEG-----WNLSHINYKELDDALEDYHYCQEVY : 239
      l      aqaen Hl      l da      g      g      y      y yc y

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Fig.2A


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*          320          *          340          *          360          *
axmi006 : RTGLKQNRDEPN-----MK-MSIFNDYRPMITITVLDIISQPSLYDIKRYRDSIGGIEVKGIKNELTRHIYTTET : 354
cry1Aa : NIGLERVUCPD-----SRDQVRYNQFRRELTLTVLDIVALFENYDSRRYP-----RTVQSOLTREIYTPV : 272
cry1Ac : NIGLERVUCPD-----SRDQVRYNQFRRELTLTVLDIVALFENYDSRRYP-----RTVQSOLTREIYTPV : 272
cry1Ia : SINGLNRGIN-----AESUVRYNQFRPDHTLTVLDIVALFENYDSRRYP-----IKTTAQLTREIYTDAT : 300
cry3Aa1 : NVGLDKLRGSS-----YESUVRYNQFRREHTLTVLDIALFFLYDVRLYP-----KEVKTETLTDFTDPI : 316
cry3Ba : NVGLNSLRGSE-----YDAQVVRFRFRREHTLTVLDLIVFFPYDVRLYS-----KGVKTETLTDFTDPI : 317
cry4Aa : KKGDLALHITPDSNLDGNIMSTYRTRTKHTTAVLDLVALFFENYVGKYP-----ICVQSELTREIYQVLN : 335
cry6Aa : QICGLPVNEQ-----QIRTHVNLSDISIFSDFSQVYDVYCSKRTS-----A-EUWAFNLYPLII : 106
cry7Aa : NSGLSRNMGST-----YEQQLNDRFRREHTLTVLDLVAFFPHOPRRYS-----DETSTOLTREIYTPV : 299
cry8Aa : KIGDKLRGSL-----SKSLNVRHOFREHTLTVLDLVALFFENYDTHMP-----DETSTAQLTREIYTPV : 310
cry10Aa : NAGLTHRTNIN-----ATUNDRYNRFRHTLTVLDLIALFFENYDPEKYP-----ICVQSELTREIYTVN : 321
cry16Aa : NKGDLDFRTAG-----QUNVRFRFRREHTLTVLDLISHPFYDARLYP-----TEVKTETLREIYSDVI : 313
cry19Ba : KSGLESKQIC-----QSDFRFRFRREHTLTVLDLVALFFENYVGKYP-----KGVKAELETRISDVI : 306
cry24Aa : TKGLNALRGST-----AIDQLFRFRREHTLTVLDLVALFFENYVVRYP-----LSTKISLSRKYTPV : 300
GL g w n r r t v i d a 5 p y y p l 4 e 6

*          380          *          400          *          420          *          440          *
axmi006 : NFDRLPQLRVQPN-----LATMEYNLTASFKLSSELEQFIETENTNFGNRLVQISNRDAPTYSN-----TI : 417
cry1Aa : LENFDGSFRG-----MAQRIQMIQ-PELMDILNSITITDVHRCFNYSCHQITASPVGFSECP--EF : 333
cry1Ac : LENFDGSFRG-----SAQCIERSIPS-PHLMIDLSSTITDAHRCFYYSCHQIHASPVGFSECP--EF : 333
cry1Ia : GTVHPHPSFTSTTWNMNAPEYSAIEAAVVRN-PHLLDFLEQVITLILLS-----RUSNTQYMMNGCH--KL : 365
cry3Aa1 : VGVNMLRGYG-----TTFSNLENVIRK-PHLDVYLRHOFHOFHOFQ-----GYGNDSFNYSCHNYST : 374
cry3Ba : FTLNALQEQY-----PTFSSIENSIRK-PHLDVYLRGHEHOFHOFHOFQ-----GYSGKDSFNYSCHNYVET : 375
cry4Aa : FEESPYKYVD-----FOYQEDSLTRPHLSTMDSDNLYEKAQITPNFFFTSHYNNHFYTLDNIS--Q : 396
cry6Aa : KSAANDIASYG-----FKVAGDPSILKDGFFKKLODEDNIVDNNSDDDAIKAIKOFKARCGILIKEAK : 170
cry7Aa : SLSISNPDIGP-----SFSQMENTAIRT-PHLDVYDEEYILTSKYKASHEIQPDLFYUSAHKVS--F : 360
cry8Aa : AFNIVTSTGFCNPNWSTHSGILEYEVENVIRP-PHLDLISSEIINTSRGG-----I-TLNDAYINYVCH--TL : 377
cry10Aa : SDTFRITILENG-----LTRN-----PILFTDINQGRFETRSR-----DILDYPDIFSFQGNQAF : 374
cry16Aa : NGEIYGLMTPYFS-----FEKASLYTRA-PHLDVYKGFREYVINSISYTFLSGGQNKYSYTNNS-S-IN : 376
cry19Ba : NDHVGLMVPYIS-----FEHAESLYTRA-PHLDVYKGFREYVINSISYTFLSGGQNKYSYTLHGET--IY : 370
cry24Aa : GRIDSPSFGDWNTG--RTLANFNDLREVTDSSESVKMLGDTITIGADISYRTPSPGDRIGVWYGNINAFYHT : 373
phlf y g

*          460          *          480          *          500          *          520          *
axmi006 : TELLYGERTGSPPTKTIRPFESYKVSIVTDQSPVPSPIQ-PHFIINQTELYLNGSSNNTLKYSAGGSLSNYQNT : 491
cry1Aa : AFPVFGNAGNAAPP-VLVSITGLGIFRLLSSPLVRRHILGSCPNNOE-LFVLDGTEFSAIITNLPSTIYRQ-- : 404
cry1Ac : TFPVFGHGNAAAPQORIVAQLGQGVYRLLSSTLVRPPFN-IGINNQO-LSVLDGTEFANG-TSSELPSAYYR-- : 403
cry1Ia : EFRITGGTLMISTQGSTINTSINPVLPFTSRDVRRTESLAGLNLFLT-OPVNGVPRVDHUKFVTHPIADNFFY : 439
cry3Aa1 : RPSIGSNDLISPPFYGKSSSEPVQNLFNCEKVRRAVANTNLAVPS-AVYSGVTKVEFSQYNDOTDEASTOTYD : 448
cry3Ba : RPSIGSNDLISPPFYGDKSIEPIQKLSFDGQKVRRTANTDIAAFPDGKIYFYGYKVDPSQYDDQKNETSTOTYD : 450
cry4Aa : KSEYFGHNVQDKLSGLATNIIYFLNVLISDNKYLDNNYSKMDFFITNGTRULEKELTAGSGQIYDVNK : 471
cry6Aa : QYEEAAKNIYSLDQFLHGDQKLEGVINIOKRLKEVQALNQAAGE-SSPAHKELLEKVKNLKTTLEKRIKAEQ : 244
cry7Aa : KKEQSNLYTIGYKTSGYISSGAYSFHGNDIQTAAAPSVVYYPY-TONYGVQVQVYGVKGVHVRGDNKY : 433
cry8Aa : KYRTADSTVYTYTANYGRITSEKNSFALEDROIDEINSTVANLANY-QKAYGVQSWHMYKRGTSSTIAYLS : 451
cry10Aa : THONDRNINUGAVHGMIIISQDTSKVFPFYRNKPIDKVEIVRHREYSDIYEMLFFSNSSEVFRYSSNSIENN-- : 448
cry16Aa : EGSFRGQDYGGSSTINIPSNVYNLWIEQYIYPWGPVYITKINFSVTDNNSKELIYGAHRNKPVVR : 451
cry19Ba : NGPFLGQDTEYGGTSSYIDISNNSYNLWTKNDEWYYPWDVYITKINFSVTDNNSKELIYGAHRNKPVVR : 445
cry24Aa : GRDQVHFRQIGDTAYEDPSTISMLYDDLYKLDLRAAAVSTIQGAMDTTFYSSSRFFDTRGNQLYQSNKP- : 447

*          540          *          560          *          580          *          600          *
axmi006 : -----TFFQFPRKDCNIVIDPGCSNFMNYSHELHFTSYVIGLQLQLDGVLCGTHSSVDRYMAISD : 560
cry1Aa : -----RGTVDSLDYITPDNSVPPRAGFSERLSEVTHLSQAAG--AVYTLRAVTESSQHRSAEFNMIPS : 467
cry1Ac : -----SGTVSLDETHPPDMNVPPRQGFSERLSEVSHFRSGFSNS-SVSIIRAPMSSQHRSAEFNMIPAS : 468
cry1Ia : PGYAGIG--TQLODSENELPPEATGPNYESYERLSEHGLISAS-----HVKALVYSQHRSAADRNTIEP : 504
cry3Aa1 : SKR---NVGAVSDSIDQAPETIDEPLEKYSSEQLNYGECFLHGS-----RGTIPVLTNTHKSVDRFMDS : 514
cry3Ba : SKRY---NGYLGADSIDQAPETIDEPLEKYSSEQLNYAECFLHQR-----RGTIFFTNTHKSVDRFMIDA : 517
cry4Aa : N-----IFGLPILKRRENGNFTLFTYDNYSEHLSFFKSLSIPAT-----YKIQVYTBATHSSVDPKATYIT : 535
cry6Aa : DLEKKVEYSFLGLPLGFPVYILENTAVQHKNOQDEKQKQDLSAQHDLDRDVKITGLHNSINTDLDNLYSQGQ : 319
cry7Aa : -----DLTYDSIDQLPPDG--EPIHERQTERUCHATAIFKATP--DYDNATIPISQTHRSAYVNRYP : 494
cry8Aa : KHTALQCTQVYESDEILDRT-VPAESYERLSEHTSHSFSKNG--SAYVCSFVYVYTHSADLNNTIYS : 523
cry10Aa : -----YKRTDSYHPIKQTKNEEYGHLSYHKTIDNYIFSVVR--ERRRVADEYTHSVDPEQNTIDL : 507
cry16Aa : -----KQGTALAKYNDQHLSEYGLINGETFGQ-----KRHGYSFAFTHSSVDPMNTIAA : 509
cry19Ba : -----TDFNFLN-----RAGNGPTTYNDVHLSYGLINGETFGQ-----KRHGYSFAFTHSSVDRYNTIHP : 503
cry24Aa : -----YPSLPITITTFGSESEGNANDSELLCDQKIQEDSSNICE-GRSSLSHATHASLDRNTILP : 512
p p h 6 s th s d n i

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Fig.2B

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      *           620           *           640           *           660           *
axmi1006 : KLTITQIPATKGNNDITNSKYTEGPGHTGGNLVYLQSQG-----RLEITTCETPNSTQSYGIRLRYATNGAGNTL : 628
cry1Aa : SCITQIPLTSTNLGSGTSSVVKCPGRTGGDILERTSPG-----QISTLRVMTAPESSQRYRVRIYASTINLQFH : 537
cry1Ac : DSITQIPAVKGNLFNGSVLS--GPGETGGDLVRLNSSGNNIQNRGYLEVPIHFPSTGIRYRVRIYASVPIHLN : 542
cry1Ia : DSITQIPLVKAFNLSSGAAVRGPGETGGDILERTINTG-----TFGDIRVMTNPPFAQRYRVRIYASTIDLQFH : 574
cry3Aa1 : KKITQIPLVKAYKQSGASVVAGPRTGGDLIOCTE-----NGSAATIVYTPDVSYSSQKYRARIYASTSQITFT : 584
cry3Ba : EKITQIPVVKAYALSSGASLLGPGGETGGMLLFKESS-----NSIAKFKVTLNSAALLQRYRVRIYASTINLRLF : 589
cry4Aa : HLITQIPAVKANSGLTAKVVOGPGHTGGDLIOFKD-----HFKITCOHSNFQSYGIRIRIYASNGSANTR : 601
cry6Aa : EAKVVFQKLOGIWAATGACDENLRITTSLOEVQSDDADEIQIELEDASDAWLVVAQEARDFILNATSPNSRONLP : 394
cry7Aa : MKITQIPAVKHYKDDPSTVVKCPGRTGGDLVIRGSTG-----YIGDIKATVNSPLSQKYRVRIYASTINVSQFN : 564
cry8Aa : DKITQIPAVKGMMLYLGGSVVQGPGETGGDILERTNPS-----ILGTFAVTVNGSLSQRYRVRIYASTIDFNT : 593
cry10Aa : DMLTQIEALKALKVSSDSEKIVKCPGHTGGDLVIRKDS-----NDFRVRLKNVSRQVRIYASTINAPKTTV : 574
cry16Aa : MKITQIPVWHAASSNGSISLEKCPGRTGGDLVIRKADS-----GLTERFKAELDKKYRVRIYKCNYSKKLI : 577
cry19Ba : DKIVQIPAVKINLVGANLIK--GPGETGGDLLELEYER-----FLSLRIK-LIASMTFRIRIYASTINISGMM : 568
cry24Aa : DSITQIPAVTAYELRCNSSSVVAGPGSTGGDLVIRSYHS-----VVSFKVYCSEKKNVRIYASTINSGNCQL : 579
      itq pa k           gpgf3gg 6           q r r rYa

      680           *           700           *           720           *           740           *
axmi1006 : PMSLTIPGVIGTPPQRLNNIFSGTINYN--MLQSGDGGGFQFPSTIVTLPLNR--NIPFIFNRADVSN--SILLIDKI : 699
cry1Aa : TSDG-----RPINQGNFSADSSGS-----MLQSGSRTVCGHTIPFNSNG-----SSVFTLSAHVFNSSGNEVYIDRI : 601
cry1Ac : MNUGN-----SSEFSNTVPAIATSLD--MLQSSDGGGFESANAFITSSLG--N--LVGVNMFAGTAGVYIDRI : 603
cry1Ia : TSING-----KALNQGNFSADNNRGE--DLQKHTRTVCGHTIPFNSLDV--QSTFTIGAWNFSSGNEVYIDRI : 638
cry3Aa1 : TSDG-----APFNQYYFDKQNNKGD--TLTVNSNRLASESAPPELGG-----NNLQIGVTCLISAGDKVYIDRI : 646
cry3Ba : YONS--NDFLVIYINKNNIDG--DLTVQIDRATSNMNGPSGD--TNDRLIGAESFVSNEKIYIDRI : 653
cry4Aa : AVINLSIPG--VAELGHALNPFTSGIDYTMKKKDQVYDESSNEVKAPNQ--NISLVFNRSDDVYNTITVLIDKI : 672
cry6Aa : DWVSDSCNCSTINMTSNQYSNPTINMTSMQVHISHEFTSLPNNFNLRN-----SNLEYKCPENNFMIVYVNS : 464
cry7Aa : VYIND--KITLQTKQNTVETLIGEGKRLTNGSGGYLNSITIOFPDE--HPKITLHLSDLSSNNSFVDSI : 631
cry8Aa : FYLG-----DTEKNRTAKMDNGA--SLVETDKFASFIIDFQDRET--QDKILLSHGDFSSGGEVYIDRI : 656
cry10Aa : FLTG-----IDTISVELPSTISRQNPATDLTMADGGVYTPRTVPNKTFEGETLLMTLYGTPNHSYNIYIDKI : 644
cry16Aa : FRKWKGE--GYIQQQIHNISSPYG--AFSYLESFTITDDENIIDLTM--EVTYPYGRQFVEDIPSLIDKI : 642
cry19Ba : INTC-----YQNPYTFNIIPPTSRD--YTELKFEDQLVDSSMISGGP--SISSENTLWLDNFSNGPVILDKI : 632
cry24Aa : MKRWPS--TCVAPRQWARHNVQGTFSNSRVEADQYEDIFITPEENN-----FAFTIDLESGGDLTIDKI : 643
      y f           1 i

      760           *           780           *           800
axmi1006 : EFLPITSSHHQNR--RKKLSTICTKINFFINHTKTL----- : 735
cry1Aa : EFLVPAEVTFEAEYD--LRAAKAVNLELTSSNQIGLKTMDVYHIDQVS : 648
cry1Ac : EFLPVIAILEAEYN--LRAAKAVNALPSTNQGLKTNVTDYHIDQVS : 650
cry1Ia : EFLVPVEVTFEAEYD--PEKADEKVTALPSTNPRGLKTMDVYHIDQVS : 685
cry3Aa1 : EFLIPVN----- : 652
cry3Ba : EFLIPVQ----- : 659
cry4Aa : EFLPITRSIREDREKOKLETVOQIITTFYANPIKNTLOSELTDYDIDQAA : 722
cry6Aa : DWYNNSDWYNN----- : 475
cry7Aa : EFLIPVDVNYAEKEK--LEKAQKAVNTLETE--GRNALQKDVTDYKVDQVS : 677
cry8Aa : EFLIPDETFEAEQD--LEAAKAVNALPSTNKD--GLRPGYTDYEVQAA : 702
cry10Aa : EFLPITLOSVDYTEKQNKETQKIWDLVN----- : 675
cry16Aa : EFLPITN----- : 648
cry19Ba : EFLPILGILNLQAQG--YDTYDQNAHGHHQNYNSNGYNNQEVNTYYQS : 679
cry24Aa : EFLIPVSGSAFEYEGKQNKETQKAVNDLEIN----- : 674
      e5 p           n

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Fig.2C

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      *      20      *      40      *      60      *
axm1007 : -----VNQN--NNVEYELIDSKNLSYPSNRNIDHSRTPYTNMNPQPCWNNYKSCDLMCCGNTQYGDNFETTS : 67
cry1Aa : -----MDNNP--NINECIPWCLSNDEVEVLGG----- : 26
cry1Ac : -----MDNNP--NINECIPWCLSNDEVEVLGG----- : 26
cry1Ia : -----NKLKNDQKHQSFSSNAKVD--KISTDS--LKEETDIEQMLDHEOCUKQSEYEN----- : 50
cry3Aa1 : MIRKGGRRKNPNMRSRSDHTTKITDME--VPTNHVQYPLAETNPPTDEDLNYKEFTIRMTADNN--TE : 63
cry3Ba : MIRKGGRRKNPNMRSRSDHTTKITDME--VPTNHVQYPLAETNPPTDEDLNYKEFTIRMTADNS--TE : 63
cry4Aa : -----NNPYQMKNEVETLMASQKKLN--ESNNYTRPPEHSKQLDQSTHYKQULNMCCQNNQQ-----YGG : 59
cry6Aa : ----- : -
cry7Aa : -----MLLNNLDGYEDSNR--TLNNSLNYPTOKALSPLQNNVQDFISHTEREQP----- : 49
cry8Aa : -----MSPNNQMEVEIDDAIPSTS--VSSDSNRFPADNPIDALQNNVQDYKMSGGENPEL-----FG : 58
cry10Aa : -----NNPYQMKNEVEITNAPSNGFS--KSNMYSRVPLANKPNQPKNNYKQULNMCCQNNQYGMN--AG : 62
cry16Aa : -----NNHYCQMEVEIDLMASNDNS--NNSHTYPRVPLAMPQDLQNNVQDYKQULNMCCGYHIENP--RE : 61
cry19Ba : -----NNSYQMKNEVEIDAKRNTC--HNSCYPKVPLAMPQNYLQNNVQDYKQULNMCCBASYAS-- : 58
cry24Aa : -----NNQYQMKNEVEIDESSQNNNN--MPNRYEADNPMAVUKKGGHYDQVNECEGSGN----- : 52
      n  cy      n      yp      p      nykd

      80      *      100      *      120      *      140      *
axm1007 : ADTIAAVSAGTIYSCGLIAGCGELTISISGPGGIIHAIHISGTHITVPFAGEQDKTVQTFKMGELFVDTPT : 142
cry1Aa : -ERIEGYTTPIDISLSITQFLISEF--VPGAGFVGLVDITUGHFGPESQ--DDAPVQIOLIHORIE : 89
cry1Ac : -ERIEGYTTPIDISLSITQFLISEF--VPGAGFVGLVDITUGHFGPESQ--DDAPVQIOLIHORIE : 89
cry1Ia : -VEPFVSASTIQTGIGLACKILGLG--VPFAGQVASLSFPLGEMLP-KG--KNQETETAEHVEITNORIS : 117
cry3Aa1 : ALDSSITKDVHOKGISVVEDLLGVVG--FDFGGAIVSFYTNPLNTLQPS--EDPKAFMEQVVALNDOKIA : 130
cry3Ba : VLDSSITKDAVGIGISVVGILLGVVG--VDFAGATSFYQSFILNATLQPS--ADPKAFMAQVEVEIDKITE : 131
cry4Aa : DFETTFIDSGELSAITVWETVLTGFG--FTTPLLALITIGGTLIPPLSTAQDQSN--TQSDETITKMLAKKEIA : 130
cry6Aa : ----- : -
cry7Aa : -EALASGHTAINTVSVDCATISALG--VPGASFITNPLKHAHLNPGNG--KI--NDEETTEVEALIDOKIE : 116
cry8Aa : NPETTFISSSTIQTGICIVGRILGALG--VDFASQASFSFPLGOLQPSKS--VDIDGEIWERVEIDVOKIE : 127
cry10Aa : NFASSETIVGSAGITVGTGILGAF--ADVLAAGTISGTLIPPLFGGSDPAN--VVQDLNIGGRPIQED : 131
cry16Aa : ASVRAGLKGKIGIVSTIVEFGGGS--IILDITGLIYQISELLEPDDTQOYTQODINHEVEDLIDKRIT : 128
cry19Ba : S--GPSQLFKYGGSIYAKILG--MIPEVGPLLSEHVSFPLFIEEKNIVVEDHDKYVAMLLKQELT : 120
cry24Aa : -ISPSPAAAITSTKIVSILVITKAKAVASSLADSKSSLGISKTHIENNV--QVSHVQVHOLITRRIQ : 117
      g  lg      p      p      w  f  e  q

      160      *      180      *      200      *      220
axm1007 : ESTPQLKQTLTEGFRQIQ--SENTADDDKILRLQAPGLPPSSALQQAALTLKIRFENVHNDPIREIPGFQLE- : 215
cry1Aa : EFARNOATSRNEGSLYQ--IYAESFREGEADPTN-----PALREHRIQONDNSALTATPLFAVON-- : 152
cry1Ac : EFARNOATSRNEGSLYQ--IYAESFREGEADPTN-----PALREHRIQONDNSALTATPLFAVON-- : 152
cry1Ia : TYARKALIDIKGLGQAJA--VHDSSESSVGCRRNN-----TRARSVVKSONIALDELIVQKLSFAVSG-- : 180
cry3Aa1 : DYARKALAEIKGLQONME--DYVSLSSQOKNPVSS--RNPHSQGRRELISQAESHRRNSHPSFAISG-- : 196
cry3Ba : EYARKALAEIKGLQONME--DYVSLSSQOKNPVNL--RSRRSQDRRELISQAESHRRNSHPSFAVSK-- : 197
cry4Aa : STYISNANKILNRSFNVIS--TYHNEHKTENMPN-----PONTQDVRTIQILVHYHEONVITELVNSCCPN : 195
cry6Aa : ----- : -
cry7Aa : EYVRKALAEIKGLGSAJD--KYOKALADILGKQDD-----PEALLSVATERIIDSLEFSHPSFKYTG-- : 179
cry8Aa : KYVRKALAEIKGLGSAJD--VHQSLEDDELEND-----ARTRSVSNORIALDLNVSSTISFAVSG-- : 190
cry10Aa : KNIIEVLTSIYTPKIQQLD--KYQEFFDKQEPARTH-----ANAKAVHDLITTEPIIDKDDHLKNNAS-- : 194
cry16Aa : EVIRGNAIRITADTGKQVD--DYNNHKKKKQDD-----KSTGNLSTIVTKETAIDSDNGAIRTNNQGSF- : 193
cry19Ba : NDTLRATSNLSGHNESLN--IYNRAIAAKQKK-----NNFASGELIRSYINDLHILSTRDQSDFSLG-- : 183
cry24Aa : ETLLLGESSINGIVAIYNRDLGAEADANNKSN-----INVQTMVAEAKTDEREFTFKRGIVRTSS-- : 182
      a      g      y  l  w      f  p

      *      240      *      260      *      280      *      300
axm1007 : -----TVKTLILPTIYQAAMHLLHLLQQGAELADEGNADIHPSHIEPNAGTSDDTYK--LLKENIPKYSNYCANTY : 284
cry1Aa : -----YQVPLLSVYVQAAMHLLHLLRDVSVFG-----QRUGEDAATNSRYN--DLTRLIGMYTDYAVROY : 211
cry1Ac : -----YQVPLLSVYVQAAMHLLHLLRDVSVFG-----QRUGEDAATNSRYN--DLTRLIGMYTDYAVROY : 211
cry1Ia : -----EEWPLLPYQAAMHLLHLLRDASTFG-----KEGCLSSSEHSTFYN--RQVERAGDYSDHCVMQY : 239
cry3Aa1 : -----VEVRLFTIYQAAMHLLHLLKDAQIYQ-----EDMGYKEDIAETVK--RQLKLTQYTDHCVKQY : 255
cry3Ba : -----FEVRLFTIYQAAMHLLHLLKDAQVFG-----EDMGYSSSEDAETVK--RQLKLTQYTDHCVKQY : 256
cry4Aa : PSDCDYVNLVLSSYQAAMHLLHLLVQAVKPEAYLKNN--RQFDPLEPLTAIDTYP--VLTKAIEDPTWYCWITY : 268
cry6Aa : -----HINDSKITLPRHSLHITKQNSNKKYQ-----PGDITNGNQ--FLSKQEGATTGANT : 51
cry7Aa : -----VEIPLLTYYQAAMHLLHLLRDSTLYG-----DKRGSTONNDEENYN--RQKKRISSEYSDHCITQY : 238
cry8Aa : -----HEVLLAVYQAAMHLLHLLRDASTFG-----EEDGETPGEISRYN--RQVQLTARYSDYCWQY : 249
cry10Aa : -----PRIPPLPAYAGIATHLNLLKHAATYNIWLON--QCINPSTFNSSNYQGYLKRKIQRYTDYCIQTY : 260
cry16Aa : -----GYELLPLPYAGIAHLLHLLRDQAQIYQ-----KQDSARANARDNTYQ--IQLEKTEFTYCYIMY : 254
cry19Ba : -----GSETVLLPSYASAAHLLHLLRDVAIYQ-----KELGYSTDEFTYF--EQKYTYTEKYSNYCWITY : 243
cry24Aa : -----SQTILLPTETQAANLHLLHLLRDVAIYQEG--UNLQSHINYSKELDDALEDTNYCYEYV : 239
      l  aqean Hl  L da      g      g      y      y  yc  y

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Fig. 3A

[illegible]

Fig. 3B

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      *           620           *           640           *           660           *
axmi007 : KHTTLPATKGNSTDTNSKVTGPGCHTGGNLVYQSQG-----RLEHTCRTFNSSTQSYIIRIRVATNGAGNTL : 626
cry1Aa : SHTTQIPLTRSTNMGSGTSVVRGPGGTGGDLIRTSFG-----QISTLRVNTAPLSQRYRVRIRVASTINLQFH : 537
cry1Ac : DSHTTQIPAVKGNFIFNGSVHS--GFGHTGGDLVRNNSGNNIQNRGYIEVPIHFPSTIRYRVRIRVASTVPIHLN : 542
cry1Ia : NSHTTQIPLVKAFNMSGGAATVRGPGGTGGDLIRRTNG-----TFGDIRVNTNPPFAQRYRVRIRVASTIDLOFH : 574
cry3Aa1 : KKITQLPLWKAYKIQSGASVWAGPRGTGGDLIQCTE-----NGSAATTVTPDVSYSQRYRVRIRVASTSQITFT : 584
cry3Ba : EKITQLPVVRYANSSGASTIEGPGGTGGDLIFKES-----NSIAKFKYTLNSAAILQRYRVRIRVASTINLRL : 589
cry4Aa : HLTTQIPAVKANSIGTASKVTGPGCHTGGDLIDFKD-----HFHTCQHSNFQDSYFIIRIRVASTGSGANTR : 601
cry6Aa : EAKVVFQKUGGIWATTGAQENLRITSLQEVQSDDADEIQIELEDASDAVLVVAQEAROFTLNASTDSRQNL : 394
cry7Aa : NKHTQIPAVHMYKDDPSITVVRGPGGTGGDLVRCSTG-----YIGDIKATVNSPISQRYRVRIRVASTVSGQFN : 564
cry8Aa : DKHTQIPAVGDMNYLGGSVVWPGPGGTGGDLIRTNPS-----ILGTFAVTNGSLSQRYRVRIRVASTIDFET : 593
cry10Aa : DNHTQIHALLKLVSSDSKIVRGPGGTGGDLVILKDS-----MDFRVRLKNVSRQVQRYRIRVASTNAPKTV : 574
cry16Aa : NKHTQIPVVKASSNGSISDERGPGGTGGDLVVRADS-----CLTRFKAEILDKKYRVRIRVASTKNSYSEKLI : 577
cry19Ba : DKHTQIPAVRINLKGAMIK--GFGHTGGDLIRVEYER-----FLSLRIK-LIASMTFRIRIRVASTISGQNM : 568
cry24Aa : DHTTQIPAVTAYEIRGNSSVWAGPGGTGGDLVMSYHS-----VUSFKYVCSELKNYRVRIRVASTHCNCQL : 579
      itq pa k           gpgf3gg 6           q r r Ya

      680           *           700           *           720           *           740           *
axmi007 : PMHSITIPGVIGPPQRLNMFSGTNYN--RQVGDGCFQFPSTVTLPLNR--NIPFFNRAQVSN-SILHEDKI : 697
cry1Aa : TSDG-----RPENQGNFSADHSSGS--MOSGERTVCFIIPFMSNG-----SSVFTUSAHVFNSSNEVYIDRI : 601
cry1Ac : VNGN-----SSSFSNTVPADATSLD--MOSSDNGCFESANASTSLG--N--LVGVRFSGTAGVILDRF : 603
cry1Ia : TSDG-----KALENQGNSADHNRGE--DLDVKIRTYCFIIPFSLDV--QSTFTIGADFFSGNEVYIDRI : 638
cry3Aa1 : TSDG-----APFQYVYDKIMKGD--ILTYASNLASTSPRELSC--NNLQGVTCLSAGDKVYIDKI : 646
cry3Ba : VQNSN-----MDFLVIYINKQMDIG--DITVQIDDEATSNMHCSSGD--TNDFTIGAESFVSNKQYIDKI : 653
cry4Aa : AVNLSIPG--VAELGNALNPTFSGIDTYMCKYKQDYECSNEVKAAPNQ--NISLVFNRSQVYVNTVILDKI : 672
cry6Aa : DMVSDSCNCSTTMTSNOYSNPTMTSMQYHLSHEVTSLPNNHLSRN--SMLEYKCPENNFTIYVQNS : 464
cry7Aa : VVIND-----KITLQTKFQNVETLIGCKDLYGSGVLEVSITIQPDE--HPKITLHLSDLNNSSFVDSI : 631
cry8Aa : LVLG-----DTEKNRFNKQMDNCA--SLVETPKAFSLIDQDRET--ODKILLNCGFSSGQEVYIDRI : 656
cry10Aa : FLTG-----IDTSVELPSTISRQNPATDLYADGQVITPRTVPNKTFEGEDTLITLYGTPNHSYNIYIDKI : 644
cry16Aa : DRKWKGE--GYIQQQIHNSIPYVG--AFSYLESFILLDENISDLTH--EVITYPYGRQFYEDIPSLIDKI : 642
cry19Ba : RVHG-----YQNPITYNIEPTTSRD-YTELKFEDQLVDLSYVSGGP--SISNTLWLNFSNGPVVLDKI : 632
cry24Aa : KRKWS--TGVAAPQARHNVQGFNSNRYEASQVLDIFITPEENN-----FAFTIDLESGGDLIDKI : 643
      y f           1 1

      760           *           780           *           800
axmi007 : EFIPHTSVVRQNR--KQRLTQIQKNTFFTNHTKNTLNIEATNYDID : 744
cry1Aa : EFVPAEVIFAEYD--LRAQKAVNLEFSSNQIGKTDVYDHDQVS : 648
cry1Ac : EFIPVIALEAYN--LRAQKAVNLEFSTNQLGKTNVYDHDQVS : 650
cry1Ia : EFVPAEVIFAEYD--FEKAQKVTALHSTNPRGKTDVYDHDQVS : 685
cry3Aa1 : EFIPVN----- : 652
cry3Ba : EFIPVQ----- : 659
cry4Aa : EFIPVTRIREDEKQKLTVDQIINTFANPIKNTLQSELTIDYDIDQAA : 722
cry6Aa : DMYNNSDUYN-- : 475
cry7Aa : EFIPVDVNYAEKEK--LEKADKAVNLEFTE-GRNALQKDYDYKVDQVS : 677
cry8Aa : EFIPVDEIFAEQD--LEAAKAVNLEFENTKD-GLRPGYDYEVNQAA : 702
cry10Aa : EFIPVTSVLDYTEKQNTKTDKIMADLVN----- : 675
cry16Aa : EFIPVN----- : 648
cry19Ba : EFIPVGIILNQAGG--YDIYDQNAHQYHQYNSNGYNYNQYNTYYQS : 679
cry24Aa : EFIPVSGSAFEYEGKQNTKTDKAVIDLIN----- : 674
      e5 p           n

```

Fig. 3C

[illegible]


```

acx1008 : STYQNYLAMYATTV--IKGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 700
cry1a : STNGSGTSS--VGGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 720
cry1ac : GPFNGSVY--S--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 740
cry1la : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 760
cry2a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 780
cry3a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 800
cry3b : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 820
cry4a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 840
cry4b : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 860
cry6a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 880
cry7a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 900
cry8a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 920
cry10a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 940
cry16a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 960
cry19a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 980
cry24a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1000
cry25a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1020
cry39a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1040
cry40a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1060
cry71a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1080
cry81a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1100
cry101a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1120
cry161a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1140
cry191a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1160
cry241a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1180
cry251a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1200
cry391a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1220
cry401a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1240
cry711a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1260
cry811a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1280
cry1011a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1300
cry1611a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1320
cry1911a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1340
cry2411a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1360
cry2511a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1380
cry3911a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1400
cry4011a : KTFSSGAAV--G--GGGTHGGGDLRPRATKSEYNAVYAGGGGILRINKKTAQGGKRRKRYRVAADKAAPTSVYVPGGGSNRFVLEKYSQNY-- 1420

```

6 5 7

6 5 7

6 5 7

6 5 7

6 5 7

Fig. 4C

```

acx1008 : REFLSSTHILEYGERDLEKTKNAQDQDLE 760
cry1a : REFLSSTHILEYGERDLEKTKNAQDQDLE 780
cry1ac : REFLSSTHILEYGERDLEKTKNAQDQDLE 800
cry1la : REFLSSTHILEYGERDLEKTKNAQDQDLE 820
cry2a : REFLSSTHILEYGERDLEKTKNAQDQDLE 840
cry3a : REFLSSTHILEYGERDLEKTKNAQDQDLE 860
cry3b : REFLSSTHILEYGERDLEKTKNAQDQDLE 880
cry4a : REFLSSTHILEYGERDLEKTKNAQDQDLE 900
cry4b : REFLSSTHILEYGERDLEKTKNAQDQDLE 920
cry6a : REFLSSTHILEYGERDLEKTKNAQDQDLE 940
cry7a : REFLSSTHILEYGERDLEKTKNAQDQDLE 960
cry8a : REFLSSTHILEYGERDLEKTKNAQDQDLE 980
cry10a : REFLSSTHILEYGERDLEKTKNAQDQDLE 1000
cry16a : REFLSSTHILEYGERDLEKTKNAQDQDLE 1020
cry19a : REFLSSTHILEYGERDLEKTKNAQDQDLE 1040
cry24a : REFLSSTHILEYGERDLEKTKNAQDQDLE 1060
cry25a : REFLSSTHILEYGERDLEKTKNAQDQDLE 1080
cry39a : REFLSSTHILEYGERDLEKTKNAQDQDLE 1100
cry40a : REFLSSTHILEYGERDLEKTKNAQDQDLE 1120

```


exmi008-orf2	20	40	60	80	100
cry19Aa-orf2	20	40	60	80	100
crybun2orf2	20	40	60	80	100
crybun3orf2	20	40	60	80	100
cry4Aa	20	40	60	80	100
cry4Ba	20	40	60	80	100
	KI L	ecidy	IDQea	5Ec65 E	Ek661 de6K AKqLSqSRN6LqNg
					W 1 6 I 1 FKGS L M GAR
exmi008-orf2	120	140	160	180	200
cry19Aa-orf2	120	140	160	180	200
crybun2orf2	120	140	160	180	200
crybun3orf2	120	140	160	180	200
cry4Aa	120	140	160	180	200
cry4Ba	120	140	160	180	200
	DI	GT6FPTVI	OKIDESKLPYTRY	VRGFGVSSKD6	16V RYGEIDa6MVP D6 Y6 P
					ce s
exmi008-orf2	220	240	260	280	300
cry19Aa-orf2	220	240	260	280	300
crybun2orf2	220	240	260	280	300
crybun3orf2	220	240	260	280	300
cry4Aa	220	240	260	280	300
cry4Ba	220	240	260	280	300
	Y C	KHV C D H F	IDTG 6DcN	N6G6 V6EKIS	PDGYA36 NLEVIEEGP6
					GEA6 VK EKKQ NE KR ETqqeYD AKQA6

Fig. 5A

axmi008-orf2	320	340	360	380	400
cry19Aa-orf2	320	340	360	380	400
crybun2orf2	320	340	360	380	400
crybun3orf2	320	340	360	380	400
cry4Aa	320	340	360	380	400
cry4Ba	320	340	360	380	400
axmi008-orf2	420	440	460	480	500
cry19Aa-orf2	420	440	460	480	500
crybun2orf2	420	440	460	480	500
crybun3orf2	420	440	460	480	500
cry4Aa	420	440	460	480	500
cry4Ba	420	440	460	480	500
axmi008-orf2	520	540	560		
cry19Aa-orf2	520	540	560		
crybun2orf2	520	540	560		
crybun3orf2	520	540	560		
cry4Aa	520	540	560		
cry4Ba	520	540	560		

Fig. 5B

Fig. 6A

Fig. 6B

```

          *           620           *           640           *           660           *
axm1009 : AVRGHGGN--IGFVH--PGFTGGHLKVSQSVHS-----LKYQAP--QRQTSVRIRIRYACLVIHGDAUFVEH : 596
cry1Aa : LTASTNDG--SGTSVWKGPGCTGGDLVRLSPG-----QISTLRVNTAPLQRVRVIRYASTTLQFHTSIDG : 542
cry1Ac : AVRGHFLF--NGSVHS--GPGCTGGDLVRLNSGNNIQMRGYIEPIHFPSTIRVRVIRYASTTLQFHTSIDG : 547
cry1Ca : LVKGFVWV--GTSVITGPGCTGGDLVRLNTFG-----DFVSLQVNSPITQVRVIRYASTTLQFHTSIDG : 539
cry1Ia : LVKAFVLS--SGAAVVRGPGCTGGDLVRLNTFG-----TFGDIRVNLDPFFAQRVRVIRYASTTLQFHTSIDG : 579
cry3Aa1 : LVKAKKLC--SGASTVAGPRITGGDLVRLNTFG-----NGSAATTVITPDVSYSORVFAPIHFPSTIRVRVIRYASTTLQFHTSIDG : 589
cry3Ba : VVKATALS--SGASTVAGPRITGGDLVRLNTFG-----NSIAKFKVTLNSAAILQRVRVIRYASTTLQFHTSIDG : 594
cry3Bb : VVKATALS--SGASTVAGPRITGGDLVRLNTFG-----NSIAKFKVTLNSAAILQRVRVIRYASTTLQFHTSIDG : 586
cry4Aa : AVKANSLG--TAKVWVGPGCTGGDLVRLNTFG-----ITCQHSNTQNSVRIRIRYASNGSANTRAVNL : 606
cry6Aa : ----- : -
cry7Aa : AVKQKQD--DPSTVWKGPGCTGGDLVRLNTFG-----YIGDIKATVNSPLSKVRVRVIRYATNVSGQFMVYND : 569
cry8Aa : AVRGDHLV--LGSVVGPGCTGGDLVRLNTFG-----ILGTFVAVTNGSLQRVRVIRYASTTLQFHTSIDG : 597
cry10Aa : ALKALKVS--SDKIDKPGCTGGDLVRLNTFG-----HDFVRVRLKQVSRQVRVIRYATNAPKTVFTLGI : 579
cry16Aa : VVKASSLN--GTSHERGPGCTGGDLVRLNTFG-----GLTERFKAELDKVRVRVIRYATNAPKTVFTLGI : 582
cry19Ba : AVKINLVG--ANIK--GPGCTGGDLVRLNTFG-----FLSLRIK-LIASVRIRIRYASNISGQFMVYND : 572
cry24Aa : AVTAYPLR--GNSVWVGPGCTGGDLVRLNTFG-----VGSFKVYCSLQVRVRVIRYASNGSANTRAVNL : 584
cry25Aa : AVTAYREHP--NIKPGCTGGDLVRLNTFG-----DILQYDLRSYDRLTEDVPEHPIKASIGVSTSTONUG : 597
cry40Aa1 : AVKATDSDTGPQVTAAGPGCTGGDLVRLNTFG-----LKLRLKASTNKNLVRVRVIRYATNAPKTVFTLGI : 584
          k           qpg tgg          i r rya

          680           *           700           *           720           *           740           *
axm1009 : S--GSSHIVSYFDCSRSRPSNTLLESDRYTDVPGITPBN--PLRYKTOFPI-----THAIDKIEFTI : 660
cry1Aa : RPNQ--NFSANSSGSNDQSGSRINQCTTPNFSNGSSVFTSAHVNSG-----NEWIDRIEFIE : 605
cry1Ac : SSIFSN--TPATATSLDNQSSDGCYFESAMATSSLGN--TGCVRNTSGT--ACVLDRIEFIE : 607
cry1Ca : ASTGVGGQVSVNMPKOKREIGENASRTORIDFNPFSRANPDIGISEQPLFGAGSISSEGLIDKIEFTI : 614
cry1Ia : KAINQ--NFSANMERGEDDQKORTVCTTPNFSNLDVQSTFTGANNFSG-----NEWIDRIEFIE : 642
cry3Aa1 : APFNQY--FDKIDKGDITVNSDLASFTPEELG--NNLQNGTGLSAG-----DKVLDKIEFTI : 650
cry3Ba : NDFLVIY--IKKIDKGDITVNSDLASFTPEELG--NNLQNGTGLSAG-----DKVLDKIEFTI : 657
cry3Bb : NDFLVIY--IKKIDKGDITVNSDLASFTPEELG--NNLQNGTGLSAG-----DKVLDKIEFTI : 649
cry4Aa : SIPGVAELG-MALNPTFGDYTDVPGITPBN--PLRYKTOFPI-----THAIDKIEFTI : 676
cry6Aa : ----- : -
cry7Aa : KITLQTKPN--TVELTGEHGDITVNSDLASFTPEELG--NNLQNGTGLSAG-----DKVLDKIEFTI : 635
cry8Aa : DTLEKN--RPMKIDKGDITVNSDLASFTPEELG--NNLQNGTGLSAG-----DKVLDKIEFTI : 660
cry10Aa : DITSVELP--S--TTSRONPHATDQYADGCVTTPRTVFNKTFEGEDTLNLTGTFN--HSYNDKIEFTI : 648
cry16Aa : GEGYQQQIHN--ISPTYG--AFSTYLSITITNENIDLVREVTYPYGRQVVEDIP--SLLDKIEFTI : 646
cry19Ba : ---YQNPITYN--IPTTSRDYTEKVEDQQLVDTSYLSGGPSISSNTDLDNFSN--PVLIDKIEFTI : 636
cry24Aa : STGVAPRQWAR--HNVGTFNSHRYEAKYLDIFITPEENN--FAFTDLESG--DVLIDKIEFTI : 647
cry25Aa : SSGPQVT--VASAASLDTKYESQVYVSPGNYTDSAPRIRLDPFG--LVDRIEFIE : 655
cry40Aa1 : P-----S-----SIISYFFLPSTGPGDSGCVYDVLVTTNPGVEIITQNDTP-----HVDKIEFTI : 639
          f           d ef p

          760           *
axm1009 : LITFPNQSLE---KREGEVNDLFIN : 682
cry1Aa : AEVTFEAEY---DLERAGAVMALIT : 628
cry1Ac : VITALEAEY---DLERAGAVMALIT : 630
cry1Ca : ADATFEAES---DLERAGAVMALIT : 637
cry1Ia : VEVTFEAEY---DLERAGAVMALIT : 665
cry3Aa1 : VQ----- : 652
cry3Ba : VQ----- : 659
cry3Bb : VQL----- : 652
cry4Aa : HTRSIREDREKQKITVQIITFEA : 702
cry6Aa : ----- : -
cry7Aa : VQVNYAEKE---KLEKAGAVMALIT : 658
cry8Aa : VQVNYAEQ---DLERAGAVMALIT : 683
cry10Aa : HTOVLDYTEKQNIETQKIVDLEV : 674
cry16Aa : TN----- : 648
cry19Ba : LGITLNOAQ---GYDTYDONANGVH : 659
cry24Aa : VSGSAFEYECKQNIETQKIVDLEV : 673
cry25Aa : VIFFPLSEQ---E---DKSVDSLEI : 674
cry40Aa1 : VNSTALEYEGKQLEKAGVQVVDLEV : 665

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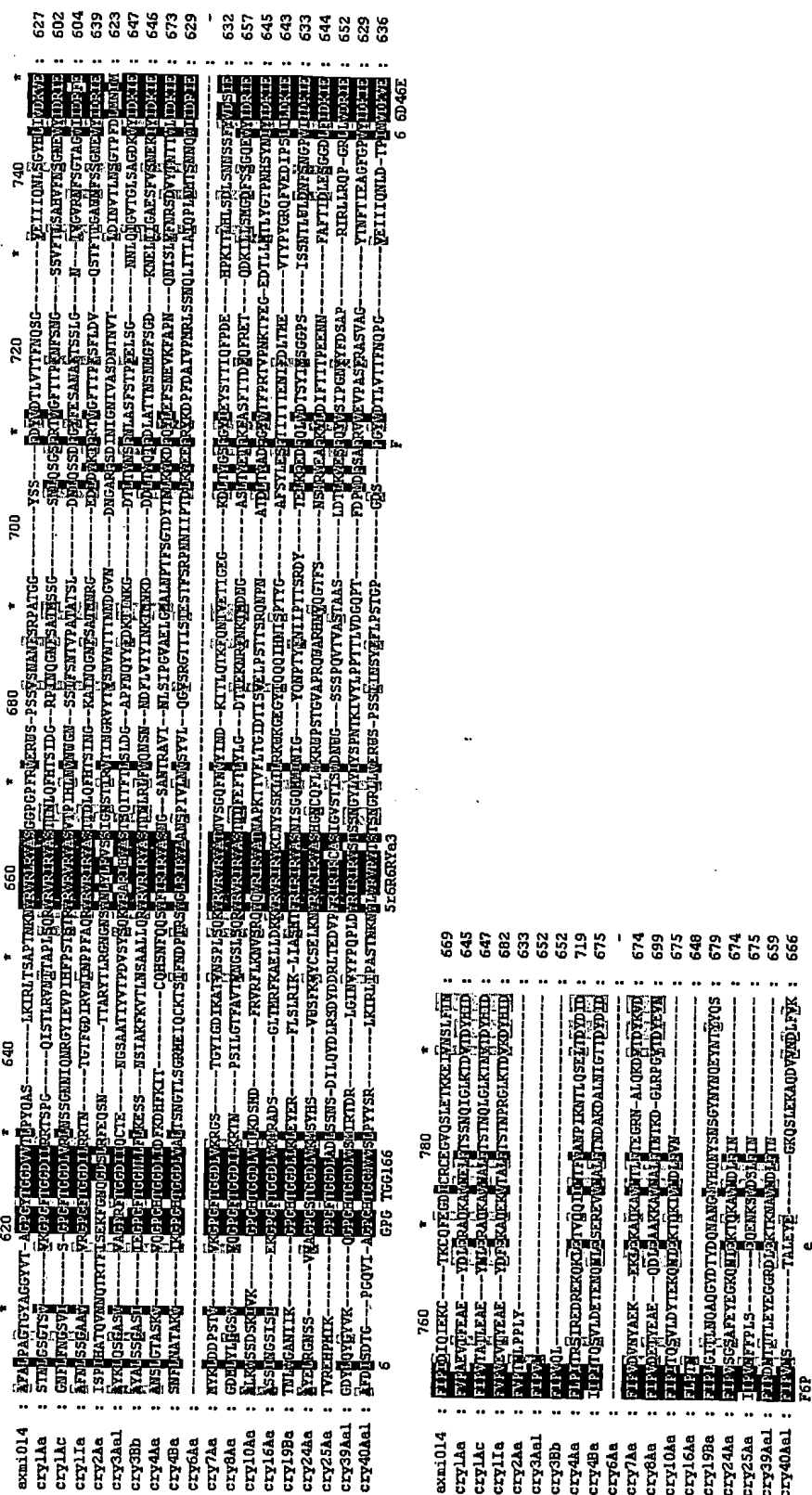
Fig. 6C

	20	40	60	80	100	120	140
exm1014	---	---	---	---	---	---	---
cry1aa	---	---	---	---	---	---	---
cry1ac	---	---	---	---	---	---	---
cry1ca	---	---	---	---	---	---	---
cry2aa	---	---	---	---	---	---	---
cry3aa	---	---	---	---	---	---	---
cry3bb	---	---	---	---	---	---	---
cry4aa	---	---	---	---	---	---	---
cry4ba	---	---	---	---	---	---	---
cry4ca	---	---	---	---	---	---	---
cry7aa	---	---	---	---	---	---	---
cry8a	---	---	---	---	---	---	---
cry10aa	---	---	---	---	---	---	---
cry16aa	---	---	---	---	---	---	---
cry19ba	---	---	---	---	---	---	---
cry24aa	---	---	---	---	---	---	---
cry25aa	---	---	---	---	---	---	---
cry39aa	---	---	---	---	---	---	---
cry42aa	---	---	---	---	---	---	---
cry40aa	---	---	---	---	---	---	---

[illegible]

Fig. 7A

[illegible]



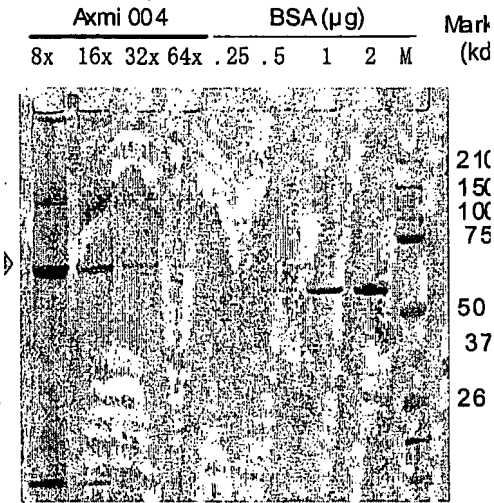


Fig. 8

SEQUENCE LISTING

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Hargiss, Tracy
Koziel, Michael G.
Duck, Nicholas B.
Carr, Brian

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Their Use

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<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2190

<212> DNA

<213> *Bacillus thuringiensis*

<400> 1

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gcatataaga aaattttttc atatataagt gaaaatattt ttgcttttct tttttttatt 180
taggataaac tttacttgta aacacaagta aatagtttat tagagataga gcctcatttt 240
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aatgatttaa gtgacgcaa tattaatatg gaacggtttg ataagaatga tgcactggaa 480
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gaattagcag gtatacaaa aaaccttgaa acatatatac aattacgtaa tgaatgggaa 720
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aatataagat cacctctata tggtagagag gcaaatacag aggttcctag agatttttat 1440
ttttatggac ccggttttta gacgttatca aagccgactc taagaccatt acagcagcct 1500
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gcaccagctc ctccttttaa ttacgtagc ttagaggag tagaattcca cactcctaca 1560
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aatccagttg ggttacctca taagggtatac agtcaccgtt tatgtcatgc aacgtttgtt 1680
cgtaaatctg ggacccttta tttacaaca ggtgccatct tttcttgac acatcgtagt 1740
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cttcgaagaa caggtcctgg aacatttgga gatatgagaa taaatattaa tgcaccatta 1920
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actttagggt ctgagggcta tagaacagta tcgttttagta ctccatttag tttctcaaat 2100
gcacaaagca tatttagatt aggtatacaa gcattttctg gagttcaaga agtttatgtg 2160
gataaaattg aatttattcc tgttgaatag 2190

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<210> 2

<211> 1890

<212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (1)...(1890)

<400> 2

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tgt ttg cta aaa ata ata aat ata gga gga aga ggt atg aat tca aag 96
Cys Leu Leu Lys Ile Ile Asn Ile Gly Gly Arg Gly Met Asn Ser Lys
20 25 30

gaa cat gat tat cta aaa gtt tgt aat gat tta agt gac gcc aat att 144
Glu His Asp Tyr Leu Lys Val Cys Asn Asp Leu Ser Asp Ala Asn Ile
35 40 45

aat atg gaa cgg ttt gat aag aat gat gca ctg gaa att ggt atg tcc 192
Asn Met Glu Arg Phe Asp Lys Asn Asp Ala Leu Glu Ile Gly Met Ser
50 55 60

att gta tct gaa ctt att ggt atg att cca ggc gga aca gct ttg caa 240
Ile Val Ser Glu Leu Ile Gly Met Ile Pro Gly Gly Thr Ala Leu Gln
65 70 75 80

ttt gtg ttt aat caa ttg tgg tct cgt tta ggt gat tct gga tgg aat 288
Phe Val Phe Asn Gln Leu Trp Ser Arg Leu Gly Asp Ser Gly Trp Asn
85 90 95

gcg ttc atg gaa cat gtg gag gaa tta att gat act aaa ata gaa ggg 336
Ala Phe Met Glu His Val Glu Glu Leu Ile Asp Thr Lys Ile Glu Gly
100 105 110

tat gca aaa aat aaa gcc tta tct gaa tta gca ggt ata caa aga aac 384
Tyr Ala Lys Asn Lys Ala Leu Ser Glu Leu Ala Gly Ile Gln Arg Asn
115 120 125

ctt gaa aca tat ata caa tta cgt aat gaa tgg gaa aat gat att gaa 432
Leu Glu Thr Tyr Ile Gln Leu Arg Asn Glu Trp Glu Asn Asp Ile Glu
130 135 140

aac tca aag gct caa ggt aag gta gct aat tac tat gaa agt ctt gag 480
Asn Ser Lys Ala Gln Gly Lys Val Ala Asn Tyr Tyr Glu Ser Leu Glu
145 150 155 160

cag gcg gtt gaa agg agt atg cct caa ttt gca gtg gag aat ttt gaa 528
Gln Ala Val Glu Arg Ser Met Pro Gln Phe Ala Val Glu Asn Phe Glu
165 170 175

gta cca ctt tta act gtc tat gtg caa gct gct aat ctt cat tta tta 576

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Leu	Leu	Arg	Asp	Val	Ser	Val	Tyr	Gly	Lys	Cys	Trp	Gly	Trp	Ser	Glu		
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cag	aaa	att	aaa	att	tat	tat	gat	aaa	cag	att	aag	tat	acc	cat	gaa	672	
Gln	Lys	Ile	Lys	Ile	Tyr	Tyr	Asp	Lys	Gln	Ile	Lys	Tyr	Thr	His	Glu		
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Tyr	Thr	Asn	His	Cys	Val	Asn	Trp	Tyr	Asn	Lys	Gly	Leu	Glu	Arg	Leu		
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Lys	Asn	Lys	Gly	Ser	Ser	Tyr	Gln	Asp	Trp	Tyr	Asn	Tyr	Asn	Arg	Phe		
			245						250					255			
cgt	aga	gaa	atg	act	ctt	act	gtt	tta	gat	atc	gtt	gct	tta	ttc	ccg	816	
Arg	Arg	Glu	Met	Thr	Leu	Thr	Val	Leu	Asp	Ile	Val	Ala	Leu	Phe	Pro		
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cac	tat	gat	gta	caa	act	tat	cca	ata	aca	acc	gtt	gct	cag	cta	aca	864	
His	Tyr	Asp	Val	Gln	Thr	Tyr	Pro	Ile	Thr	Thr	Val	Ala	Gln	Leu	Thr		
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agg	gaa	gtt	tat	acg	gat	cct	tta	ctt	aat	ttt	aat	cct	aaa	tta	cat	912	
Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Leu	Asn	Phe	Asn	Pro	Lys	Leu	His		
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Ser	Val	Ser	Gln	Leu	Pro	Ser	Phe	Ser	Asp	Met	Glu	Asn	Ala	Thr	Ile		
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aga	act	cca	cat	ctg	atg	gaa	ttt	tta	aga	atg	cta	aca	att	tat	aca	1008	
Arg	Thr	Pro	His	Leu	Met	Glu	Phe	Leu	Arg	Met	Leu	Thr	Ile	Tyr	Thr		
				325					330					335			
gat	tg	tat	agt	gtg	gga	aga	aac	tat	tat	tg	gga	gga	cat	cgc	gtg	1056	
Asp	Trp	Tyr	Ser	Val	Gly	Arg	Asn	Tyr	Tyr	Trp	Gly	Gly	His	Arg	Val		
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Thr	Ser	Tyr	His	Val	Gly	Gly	Glu	Asn	Ile	Arg	Ser	Pro	Leu	Tyr	Gly		
		355					360					365					
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Arg	Glu	Ala	Asn	Gln	Glu	Val	Pro	Arg	Asp	Phe	Tyr	Phe	Tyr	Gly	Pro		
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Val	Phe	Lys	Thr	Leu	Ser	Lys	Pro	Thr	Leu	Arg	Pro	Leu	Gln	Gln	Pro		
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Ala	Pro	Ala	Pro	Pro	Phe	Asn	Leu	Arg	Ser	Leu	Glu	Gly	Val	Glu	Phe		
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cac	act	cct	aca	ggt	agt	ttt	atg	tat	cgt	gaa	aga	gga	tcg	gta	gat	1296	
His	Thr	Pro	Thr	Gly	Ser	Phe	Met	Tyr	Arg	Glu	Arg	Gly	Ser	Val	Asp		
			420					425					430				
tct	ttt	aat	gag	ttg	ccg	cct	ttt	aat	cca	gtt	ggg	tta	cct	cat	aag	1344	
Ser	Phe	Asn	Glu	Leu	Pro	Pro	Phe	Asn	Pro	Val	Gly	Leu	Pro	His	Lys		
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Val Tyr Ser His Arg Leu Cys His Ala Thr Phe Val Arg Lys Ser Gly
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acc cct tat tta aca aca ggt gcc atc ttt tct tgg aca cat cgt agt 1440
 Thr Pro Tyr Leu Thr Gly Ala Ile Phe Ser Trp Thr His Arg Ser
 465 470 475 480

gct gaa gaa acc aat aca att gaa tca aat att att acg caa atc ccg 1488
 Ala Glu Glu Thr Asn Thr Ile Glu Ser Asn Ile Ile Thr Gln Ile Pro
 485 490 495

tta gta aaa gca tat caa att ggg tca ggc act act gta agg aaa gga 1536
 Leu Val Lys Ala Tyr Gln Ile Gly Ser Gly Thr Thr Val Arg Lys Gly
 500 505 510

cca gga ttc aca gga ggg gat ata ctt cga aga aca ggt cct gga aca 1584
 Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Gly Pro Gly Thr
 515 520 525

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 Phe Gly Asp Met Arg Ile Asn Ile Asn Ala Pro Leu Ser Gln Arg Tyr
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cgt gta agg att cgt tat gct tct acg aca gat tta caa ttt gtc acg 1680
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 545 550 555 560

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 565 570 575

aat aat cta aat act tta ggt tct gag ggc tat aga aca gta tcg ttt 1776
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 580 585 590

agt act cca ttt agt ttc tca aat gca caa agc ata ttt aga tta ggt 1824
 Ser Thr Pro Phe Ser Phe Ser Asn Ala Gln Ser Ile Phe Arg Leu Gly
 595 600 605

ata caa gca ttt tct gga gtt caa gaa gtt tat gtg gat aaa att gaa 1872
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ttt att cct gtt gaa tag 1890
 Phe Ile Pro Val Glu *

<210> 3

<211> 629

<212> PRT

<213> Bacillus thuringiensis

<400> 3

Met Ser Glu Leu Lys Gly Lys Phe Lys Lys Ser Thr Asn Arg Thr Cys
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Cys Leu Leu Lys Ile Ile Asn Ile Gly Gly Arg Gly Met Asn Ser Lys
 20 25 30

Glu His Asp Tyr Leu Lys Val Cys Asn Asp Leu Ser Asp Ala Asn Ile
 35 40 45

Asn Met Glu Arg Phe Asp Lys Asn Asp Ala Leu Glu Ile Gly Met Ser
 50 55 60

Ile Val Ser Glu Leu Ile Gly Met Ile Pro Gly Gly Thr Ala Leu Gln
 65 70 75 80

Phe Val Phe Asn Gln Leu Trp Ser Arg Leu Gly Asp Ser Gly Trp Asn
 85 90 95

Ala Phe Met Glu His Val Glu Glu Leu Ile Asp Thr Lys Ile Glu Gly
 100 105 110

Tyr Ala Lys Asn Lys Ala Leu Ser Glu Leu Ala Gly Ile Gln Arg Asn
 115 120 125
 Leu Glu Thr Tyr Ile Gln Leu Arg Asn Glu Trp Glu Asn Asp Ile Glu
 130 135 140
 Asn Ser Lys Ala Gln Gly Lys Val Ala Asn Tyr Tyr Glu Ser Leu Glu
 145 150 155 160
 Gln Ala Val Glu Arg Ser Met Pro Gln Phe Ala Val Glu Asn Phe Glu
 165 170 175
 Val Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn Leu His Leu Leu
 180 185 190
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 195 200 205
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 245 250 255
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 260 265 270
 His Tyr Asp Val Gln Thr Tyr Pro Ile Thr Thr Val Ala Gln Leu Thr
 275 280 285
 Arg Glu Val Tyr Thr Asp Pro Leu Leu Asn Phe Asn Pro Lys Leu His
 290 295 300
 Ser Val Ser Gln Leu Pro Ser Phe Ser Asp Met Glu Asn Ala Thr Ile
 305 310 315 320
 Arg Thr Pro His Leu Met Glu Phe Leu Arg Met Leu Thr Ile Tyr Thr
 325 330 335
 Asp Trp Tyr Ser Val Gly Arg Asn Tyr Tyr Trp Gly Gly His Arg Val
 340 345 350
 Thr Ser Tyr His Val Gly Gly Glu Asn Ile Arg Ser Pro Leu Tyr Gly
 355 360 365
 Arg Glu Ala Asn Gln Glu Val Pro Arg Asp Phe Tyr Phe Tyr Gly Pro
 370 375 380
 Val Phe Lys Thr Leu Ser Lys Pro Thr Leu Arg Pro Leu Gln Gln Pro
 385 390 395 400
 Ala Pro Ala Pro Pro Phe Asn Leu Arg Ser Leu Glu Gly Val Glu Phe
 405 410 415
 His Thr Pro Thr Gly Ser Phe Met Tyr Arg Glu Arg Gly Ser Val Asp
 420 425 430
 Ser Phe Asn Glu Leu Pro Pro Phe Asn Pro Val Gly Leu Pro His Lys
 435 440 445
 Val Tyr Ser His Arg Leu Cys His Ala Thr Phe Val Arg Lys Ser Gly
 450 455 460
 Thr Pro Tyr Leu Thr Thr Gly Ala Ile Phe Ser Trp Thr His Arg Ser
 465 470 475 480
 Ala Glu Glu Thr Asn Thr Ile Glu Ser Asn Ile Ile Thr Gln Ile Pro
 485 490 495
 Leu Val Lys Ala Tyr Gln Ile Gly Ser Gly Thr Thr Val Arg Lys Gly
 500 505 510
 Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Gly Pro Gly Thr
 515 520 525
 Phe Gly Asp Met Arg Ile Asn Ile Asn Ala Pro Leu Ser Gln Arg Tyr
 530 535 540
 Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Val Thr
 545 550 555 560
 Ser Ile Asn Gly Thr Thr Ile Asn Ile Gly Asn Phe Pro Lys Thr Ile
 565 570 575
 Asn Asn Leu Asn Thr Leu Gly Ser Glu Gly Tyr Arg Thr Val Ser Phe
 580 585 590
 Ser Thr Pro Phe Ser Phe Ser Asn Ala Gln Ser Ile Phe Arg Leu Gly
 595 600 605
 Ile Gln Ala Phe Ser Gly Val Gln Glu Val Tyr Val Asp Lys Ile Glu
 610 615 620
 Phe Ile Pro Val Glu
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<210> 4
 <211> 1806
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> CDS
 <222> (1)...(1806)

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 gac gcc aat att aat atg gaa cgg ttt gat aag aat gat gca ctg gaa 96
 Asp Ala Asn Ile Asn Met Glu Arg Phe Asp Lys Asn Asp Ala Leu Glu
 20 25 30
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 Ile Gly Met Ser Ile Val Ser Glu Leu Ile Gly Met Ile Pro Gly Gly
 35 40 45
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 Thr Ala Leu Gln Phe Val Phe Asn Gln Leu Trp Ser Arg Leu Gly Asp
 50 55 60
 tct gga tgg aat gcg ttc atg gaa cat gtg gag gaa tta att gat act 240
 Ser Gly Trp Asn Ala Phe Met Glu His Val Glu Glu Leu Ile Asp Thr
 65 70 75 80
 aaa ata gaa ggg tat gca aaa aat aaa gcc tta tct gaa tta gca ggt 288
 Lys Ile Glu Gly Tyr Ala Lys Asn Lys Ala Leu Ser Glu Leu Ala Gly
 85 90 95
 ata caa aga aac ctt gaa aca tat ata caa tta cgt aat gaa tgg gaa 336
 Ile Gln Arg Asn Leu Glu Thr Tyr Ile Gln Leu Arg Asn Glu Trp Glu
 100 105 110
 aat gat att gaa aac tca aag gct caa ggt aag gta gct aat tac tat 384
 Asn Asp Ile Glu Asn Ser Lys Ala Gln Gly Lys Val Ala Asn Tyr Tyr
 115 120 125
 gaa agt ctt gag cag gcg gtt gaa agg agt atg cct caa ttt gca gtg 432
 Glu Ser Leu Glu Gln Ala Val Glu Arg Ser Met Pro Gln Phe Ala Val
 130 135 140
 gag aat ttt gaa gta cca ctt tta act gtc tat gtg caa gct gct aat 480
 Glu Asn Phe Glu Val Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn
 145 150 155 160
 ctt cat tta tta tta tta aga gat gtt tca gtt tat gga aag tgt tgg 528
 Leu His Leu Leu Leu Leu Arg Asp Val Ser Val Tyr Gly Lys Cys Trp
 165 170 175
 gga tgg tcg gag cag aaa att aaa att tat tat gat aaa cag att aag 576
 Gly Trp Ser Glu Gln Lys Ile Lys Ile Tyr Tyr Asp Lys Gln Ile Lys
 180 185 190
 tat acc cat gaa tac aca aat cat tgt gta aat tgg tat aat aaa gga 624
 Tyr Thr His Glu Tyr Thr Asn His Cys Val Asn Trp Tyr Asn Lys Gly
 195 200 205
 ctt gag aga tta aaa aat aaa ggt tct tct tat caa gat tgg tac aat 672
 Leu Glu Arg Leu Lys Asn Lys Gly Ser Ser Tyr Gln Asp Trp Tyr Asn
 210 215 220
 tat aat cgt ttc cgt aga gaa atg act ctt act gtt tta gat atc gtt 720
 Tyr Asn Arg Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Ile Val

225	230	235	240	
gct tta ttc ccg cac tat gat gta caa act tat cca ata aca acc gtt				768
Ala Leu Phe Pro His Tyr Asp Val Gln Thr Tyr Pro Ile Thr Thr Val				
	245	250	255	
gct cag cta aca agg gaa gtt tat acg gat cct tta ctt aat ttt aat				816
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Leu Asn Phe Asn				
	260	265	270	
cct aaa tta cat tct gtg tct caa tta cct agt ttt agt gac atg gaa				864
Pro Lys Leu His Ser Val Ser Gln Leu Pro Ser Phe Ser Asp Met Glu				
	275	280	285	
aat gca aca att aga act cca cat ctg atg gaa ttt tta aga atg cta				912
Asn Ala Thr Ile Arg Thr Pro His Leu Met Glu Phe Leu Arg Met Leu				
	290	295	300	
aca att tat aca gat tgg tat agt gtg gga aga aac tat tat tgg gga				960
Thr Ile Tyr Thr Asp Trp Tyr Ser Val Gly Arg Asn Tyr Tyr Trp Gly				
	305	310	315	320
gga cat cgc gtg acg tct tac cat gta gga gga gag aat ata aga tca				1008
Gly His Arg Val Thr Ser Tyr His Val Gly Gly Glu Asn Ile Arg Ser				
	325	330	335	
cct cta tat ggt aga gag gca aat caa gag gtt cct aga gat ttt tat				1056
Pro Leu Tyr Gly Arg Glu Ala Asn Gln Glu Val Pro Arg Asp Phe Tyr				
	340	345	350	
ttt tat gga ccc gtt ttt aag acg tta tca aag ccg act cta aga cca				1104
Phe Tyr Gly Pro Val Phe Lys Thr Leu Ser Lys Pro Thr Leu Arg Pro				
	355	360	365	
tta cag cag cct gca cca gct cct cct ttt aat tta cgt agc tta gag				1152
Leu Gln Gln Pro Ala Pro Ala Pro Pro Phe Asn Leu Arg Ser Leu Glu				
	370	375	380	
gga gta gaa ttc cac act cct aca ggt agt ttt atg tat cgt gaa aga				1200
Gly Val Glu Phe His Thr Pro Thr Gly Ser Phe Met Tyr Arg Glu Arg				
	385	390	395	400
gga tcg gta gat tct ttt aat gag ttg ccg cct ttt aat cca gtt ggg				1248
Gly Ser Val Asp Ser Phe Asn Glu Leu Pro Pro Phe Asn Pro Val Gly				
	405	410	415	
tta cct cat aag gta tac agt cac cgt tta tgt cat gca acg ttt gtt				1296
Leu Pro His Lys Val Tyr Ser His Arg Leu Cys His Ala Thr Phe Val				
	420	425	430	
cgt aaa tct ggg acc cct tat tta aca aca ggt gcc atc ttt tct tgg				1344
Arg Lys Ser Gly Thr Pro Tyr Leu Thr Thr Gly Ala Ile Phe Ser Trp				
	435	440	445	
aca cat cgt agt gct gaa gaa acc aat aca att gaa tca aat att att				1392
Thr His Arg Ser Ala Glu Glu Thr Asn Thr Ile Glu Ser Asn Ile Ile				
	450	455	460	
acg caa atc ccg tta gta aaa gca tat caa att ggg tca ggc act act				1440
Thr Gln Ile Pro Leu Val Lys Ala Tyr Gln Ile Gly Ser Gly Thr Thr				
	465	470	475	480
gta agg aaa gga cca gga ttc aca gga ggg gat ata ctt cga aga aca				1488
Val Arg Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr				
	485	490	495	
ggg cct gga aca ttt gga gat atg aga ata aat att aat gca cca tta				1536
Gly Pro Gly Thr Phe Gly Asp Met Arg Ile Asn Ile Asn Ala Pro Leu				

500	505	510	
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Ser Gln Arg Tyr Arg Val Arg Ile	Arg Tyr Ala Ser Thr Thr Asp Leu		
515	520	525	
caa ttt gtc acg agt att aat ggg acc acc att aat att ggt aac ttc	1632		
Gln Phe Val Thr Ser Ile Asn Gly Thr Thr Ile Asn Ile Gly Asn Phe			
530	535	540	
ccg aaa act att aat aat cta aat act tta ggt tct gag ggc tat aga	1680		
Pro Lys Thr Ile Asn Asn Leu Asn Thr Leu Gly Ser Glu Gly Tyr Arg			
545	550	555	
aca gta tcg ttt agt act cca ttt agt ttc tca aat gca caa agc ata	1728		
Thr Val Ser Phe Ser Thr Pro Phe Ser Phe Ser Asn Ala Gln Ser Ile			
565	570	575	
ttt aga tta ggt ata caa gca ttt tct gga gtt caa gaa gtt tat gtg	1776		
Phe Arg Leu Gly Ile Gln Ala Phe Ser Gly Val Gln Glu Val Tyr Val			
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595	600		

<210> 5

<211> 601

<212> PRT

<213> *Bacillus thuringiensis*

<400> 5

Met Asn Ser Lys Glu His Asp Tyr Leu Lys Val Cys Asn Asp Leu Ser	
1 5 10 15	
Asp Ala Asn Ile Asn Met Glu Arg Phe Asp Lys Asn Asp Ala Leu Glu	
20 25 30	
Ile Gly Met Ser Ile Val Ser Glu Leu Ile Gly Met Ile Pro Gly Gly	
35 40 45	
Thr Ala Leu Gln Phe Val Phe Asn Gln Leu Trp Ser Arg Leu Gly Asp	
50 55 60	
Ser Gly Trp Asn Ala Phe Met Glu His Val Glu Leu Ile Asp Thr	
65 70 75 80	
Lys Ile Glu Gly Tyr Ala Lys Asn Lys Ala Leu Ser Glu Leu Ala Gly	
85 90 95	
Ile Gln Arg Asn Leu Glu Thr Tyr Ile Gln Leu Arg Asn Glu Trp Glu	
100 105 110	
Asn Asp Ile Glu Asn Ser Lys Ala Gln Gly Lys Val Ala Asn Tyr Tyr	
115 120 125	
Glu Ser Leu Glu Gln Ala Val Glu Arg Ser Met Pro Gln Phe Ala Val	
130 135 140	
Glu Asn Phe Glu Val Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn	
145 150 155 160	
Leu His Leu Leu Leu Leu Arg Asp Val Ser Val Tyr Gly Lys Cys Trp	
165 170 175	
Gly Trp Ser Glu Gln Lys Ile Lys Ile Tyr Tyr Asp Lys Gln Ile Lys	
180 185 190	
Tyr Thr His Glu Tyr Thr Asn His Cys Val Asn Trp Tyr Asn Lys Gly	
195 200 205	
Leu Glu Arg Leu Lys Asn Lys Gly Ser Ser Tyr Gln Asp Trp Tyr Asn	
210 215 220	
Tyr Asn Arg Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Ile Val	
225 230 235 240	
Ala Leu Phe Pro His Tyr Asp Val Gln Thr Tyr Pro Ile Thr Thr Val	
245 250 255	
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Leu Asn Phe Asn	
260 265 270	
Pro Lys Leu His Ser Val Ser Gln Leu Pro Ser Phe Ser Asp Met Glu	

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      275              280              285
Asn Ala Thr Ile Arg Thr Pro His Leu Met Glu Phe Leu Arg Met Leu
  290              295              300
Thr Ile Tyr Thr Asp Trp Tyr Ser Val Gly Arg Asn Tyr Tyr Trp Gly
 305              310              315              320
Gly His Arg Val Thr Ser Tyr His Val Gly Gly Glu Asn Ile Arg Ser
      325              330              335
Pro Leu Tyr Gly Arg Glu Ala Asn Gln Glu Val Pro Arg Asp Phe Tyr
  340              345              350
Phe Tyr Gly Pro Val Phe Lys Thr Leu Ser Lys Pro Thr Leu Arg Pro
      355              360              365
Leu Gln Gln Pro Ala Pro Ala Pro Pro Phe Asn Leu Arg Ser Leu Glu
  370              375              380
Gly Val Glu Phe His Thr Pro Thr Gly Ser Phe Met Tyr Arg Glu Arg
 385              390              395              400
Gly Ser Val Asp Ser Phe Asn Glu Leu Pro Pro Phe Asn Pro Val Gly
      405              410              415
Leu Pro His Lys Val Tyr Ser His Arg Leu Cys His Ala Thr Phe Val
  420              425              430
Arg Lys Ser Gly Thr Pro Tyr Leu Thr Thr Gly Ala Ile Phe Ser Trp
      435              440              445
Thr His Arg Ser Ala Glu Glu Thr Asn Thr Ile Glu Ser Asn Ile Ile
  450              455              460
Thr Gln Ile Pro Leu Val Lys Ala Tyr Gln Ile Gly Ser Gly Thr Thr
 465              470              475              480
Val Arg Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr
      485              490              495
Gly Pro Gly Thr Phe Gly Asp Met Arg Ile Asn Ile Asn Ala Pro Leu
  500              505              510
Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu
      515              520              525
Gln Phe Val Thr Ser Ile Asn Gly Thr Thr Ile Asn Ile Gly Asn Phe
  530              535              540
Pro Lys Thr Ile Asn Asn Leu Asn Thr Leu Gly Ser Glu Gly Tyr Arg
 545              550              555              560
Thr Val Ser Phe Ser Thr Pro Phe Ser Phe Ser Asn Ala Gln Ser Ile
      565              570              575
Phe Arg Leu Gly Ile Gln Ala Phe Ser Gly Val Gln Glu Val Tyr Val
  580              585              590
Asp Lys Ile Glu Phe Ile Pro Val Glu
 595              600

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<210> 6
 <211> 2208
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> CDS
 <222> (1)...(2208)

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<400> 6
atg aat caa aat aac gat aat aac gaa tat gaa att att gat tcg cat   48
Met Asn Gln Asn Asn Asp Asn Asn Glu Tyr Glu Ile Ile Asp Ser His
  1              5              10              15

acc tca cct tat ttt ccg aac aga aac agt aat gat tct aga tac cct   96
Thr Ser Pro Tyr Phe Pro Asn Arg Asn Ser Asn Asp Ser Arg Tyr Pro
      20              25              30

tac aca aat aat cca aat caa cca tta caa aac aca aat tac aaa gag   144
Tyr Thr Asn Asn Pro Asn Gln Pro Leu Gln Asn Thr Asn Tyr Lys Glu
      35              40              45

tgg ctc aat atg tgt caa ggg aat aca caa tat ggt gat aat ttc gag   192
Trp Leu Asn Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu
  50              55              60

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aca ttt gct agt gct gat aca att gct gca gtt agt gca ggt act att 240
 Thr Phe Ala Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile
 65 70 75 80

gta tcc ggt act ctg tta gcc ggt ata ggt ggg ctc act tct ata tcc 288
 Val Ser Gly Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser
 85 90 95

gga ccg ata gga ata ata ggt gct ata ata ata tct ttt ggt acc cta 336
 Gly Pro Ile Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu
 100 105 110

atc act gtc ttt tgg ccc gcg gga gaa caa gac aaa aca gta tgg aca 384
 Ile Thr Val Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr
 115 120 125

caa ttt att aaa atg gga gaa att ttt gtt gat aca ccg tta aca gaa 432
 Gln Phe Ile Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu
 130 135 140

agc ata aaa cag cta aag tta caa act tta gaa gga ttt aga caa ata 480
 Ser Ile Lys Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile
 145 150 155 160

tta caa agc tat aat aca gca tta gat gat tgg aga aaa tta aaa aga 528
 Leu Gln Ser Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg
 165 170 175

cta caa gct cct gga tta cca cca tca tca gca tta caa caa gct gcc 576
 Leu Gln Ala Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala
 180 185 190

ttg act ctt aaa ata cga ttt gag aat gtt cac aat gat ttt att cga 624
 Leu Thr Leu Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg
 195 200 205

gaa ata cct ggt ttc caa ctt gaa act tat aaa acg cta tta cta cct 672
 Glu Ile Pro Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro
 210 215 220

att tat gcg caa gct gct aat ttt cat tta aat tta tta caa caa ggt 720
 Ile Tyr Ala Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly
 225 230 235 240

gct gaa ttg gct gat gaa tgg aat gca gat ata cat cct tca caa att 768
 Ala Glu Leu Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile
 245 250 255

gaa cct aat gct gga aca tca gat gac tat tat aaa ctt tta aaa gaa 816
 Glu Pro Asn Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu
 260 265 270

aat ata cct aaa tat agt aac tat tgt gca aat acc tat aga aca gga 864
 Asn Ile Pro Lys Tyr Ser Asn Tyr Cys Ala Asn Thr Tyr Arg Thr Gly
 275 280 285

cta aaa aat ctt aga gac gaa cca aat atg aaa tgg agt ata ttt aat 912
 Leu Lys Asn Leu Arg Asp Glu Pro Asn Met Lys Trp Ser Ile Phe Asn
 290 295 300

gac tat cga aga tat atg acc att act gta tta gat acc atc tct caa 960
 Asp Tyr Arg Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ser Gln
 305 310 315 320

ttt tct tta tat gat ata aaa aga tat aga gat tca ata gga gga ata 1008
 Phe Ser Leu Tyr Asp Ile Lys Arg Tyr Arg Asp Ser Ile Gly Gly Ile
 325 330 335

gaa gta aaa ggc att aag aat gaa ctc aca aga gaa att tat aca act 1056
 Glu Val Lys Gly Ile Lys Asn Glu Leu Thr Arg Glu Ile Tyr Thr Thr
 340 345 350

gaa ata aat ttt gat cgt ctt cct caa ctt aga gtt caa ccc aat cta 1104
 Glu Ile Asn Phe Asp Arg Leu Pro Gln Leu Arg Val Gln Pro Asn Leu
 355 360 365

gct acg atg gaa tat aat tta aca cgt gca agt ttt aaa tta ttt tca 1152
 Ala Thr Met Glu Tyr Asn Leu Thr Arg Ala Ser Phe Lys Leu Phe Ser
 370 375 380

ttt tta gaa caa ttt att ttt tat aca gaa aat aca aat ttc ggg aat 1200
 Phe Leu Glu Gln Phe Ile Phe Tyr Thr Glu Asn Thr Asn Phe Gly Asn
 385 390 395 400

cgt tta gtt ggt att tct aat cgt gat gca cct act tat agc aat act 1248
 Arg Leu Val Gly Ile Ser Asn Arg Asp Ala Pro Thr Tyr Ser Asn Thr
 405 410 415

ata act gaa act tta tat gga gaa aga aca ggt tca ccc aca aca aaa 1296
 Ile Thr Glu Thr Leu Tyr Gly Glu Arg Thr Gly Ser Pro Thr Thr Lys
 420 425 430

aca ata aga cca ttt gaa tct tat aaa gtt tca att gta act gat aga 1344
 Thr Ile Arg Pro Phe Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg
 435 440 445

caa tca cct cct gtt tcc cct att caa cca cac ttt ata att aat caa 1392
 Gln Ser Pro Pro Val Ser Pro Ile Gln Pro His Phe Ile Ile Asn Gln
 450 455 460

att gaa ctt tat tta aat ggc tca tct aac aac aca ctc aaa tat tca 1440
 Ile Glu Leu Tyr Leu Asn Gly Ser Ser Asn Asn Thr Leu Lys Tyr Ser
 465 470 475 480

gca gga ggg tct tta tct aat tat caa aac aca act ttt ttt caa ttt 1488
 Ala Gly Gly Ser Leu Ser Asn Tyr Gln Asn Thr Thr Phe Phe Gln Phe
 485 490 495

cct aga aaa aaa gac tgc aat cta gtt att gat cca ggt tgt tca cca 1536
 Pro Arg Lys Lys Asp Cys Asn Leu Val Ile Asp Pro Gly Cys Ser Pro
 500 505 510

aac ttt aat aac tat agt cat att tta tcc cat ttt tca tta ttt act 1584
 Asn Phe Asn Asn Tyr Ser His Ile Leu Ser His Phe Ser Leu Phe Thr
 515 520 525

tat tcc tat gtg att gga tta cag cta caa ata tta gat aca ggt gta 1632
 Tyr Ser Tyr Val Ile Gly Leu Gln Leu Gln Ile Leu Asp Thr Gly Val
 530 535 540

tta gga tgg aca cac agt agt gtt gat aga tat aat gca ata tca gat 1680
 Leu Gly Trp Thr His Ser Ser Val Asp Arg Tyr Asn Ala Ile Ser Asp
 545 550 555 560

aaa ata att aca atg atc cca gca atc aaa ggt aac aat ctt gat aca 1728
 Lys Ile Ile Thr Met Ile Pro Ala Ile Lys Gly Asn Asn Leu Asp Thr
 565 570 575

aac tct aag gta att gaa gga cct ggt cat aca gga gga aac ttg gtt 1776
 Asn Ser Lys Val Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val
 580 585 590

tat tta caa agt caa ggg cgt tta gaa att aca tgt gaa act cct aat 1824
 Tyr Leu Gln Ser Gln Gly Arg Leu Glu Ile Thr Cys Glu Thr Pro Asn
 595 600 605

tct aca caa tct tat ttc att aga ctt cga tat gct aca aat ggt gct 1872
 Ser Thr Gln Ser Tyr Phe Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala
 610 615 620

gga aat act ctt cct aat ata tct ctt aca ata cca gga gta ata gga 1920
 Gly Asn Thr Leu Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly
 625 630 635 640

ata cca cct caa cga ctc aac aac act ttt tct ggt aca aat tat aat 1968
 Ile Pro Pro Gln Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn
 645 650 655

aat tta caa tac gga gat ttt ggg tat ttc caa ttt cca agt aca gta 2016
 Asn Leu Gln Tyr Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val
 660 665 670

aca tta cct tta aat cga aac ata cca ttt ata ttt aat cgt gca gat 2064
 Thr Leu Pro Leu Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp
 675 680 685

gta tca aat tca att tta atc att gat aaa att gaa ttt ata cca att 2112
 Val Ser Asn Ser Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile
 690 695 700

act tcc tct atg cac caa aat aga gaa aaa caa aaa tta gaa act atc 2160
 Thr Ser Ser Met His Gln Asn Arg Glu Lys Gln Lys Leu Glu Thr Ile
 705 710 715 720

caa aca aaa ata aat aca ttt ttc aca aat cat aca aaa aca ctt tga 2208
 Gln Thr Lys Ile Asn Thr Phe Phe Thr Asn His Thr Lys Thr Leu *
 725 730 735

<210> 7

<211> 735

<212> PRT

<213> Bacillus thuringiensis

<400> 7

Met Asn Gln Asn Asn Asp Asn Asn Glu Tyr Glu Ile Ile Asp Ser His
 1 5 10 15
 Thr Ser Pro Tyr Phe Pro Asn Arg Asn Ser Asn Asp Ser Arg Tyr Pro
 20 25 30
 Tyr Thr Asn Asn Pro Asn Gln Pro Leu Gln Asn Thr Asn Tyr Lys Glu
 35 40 45
 Trp Leu Asn Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu
 50 55 60
 Thr Phe Ala Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile
 65 70 75 80
 Val Ser Gly Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser
 85 90 95
 Gly Pro Ile Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu
 100 105 110
 Ile Thr Val Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr
 115 120 125
 Gln Phe Ile Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu
 130 135 140
 Ser Ile Lys Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile
 145 150 155 160
 Leu Gln Ser Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg
 165 170 175
 Leu Gln Ala Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala
 180 185 190
 Leu Thr Leu Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg
 195 200 205
 Glu Ile Pro Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro

210	215	220
Ile Tyr Ala Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly		
225	230	235
Ala Glu Leu Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile		
	245	250
Glu Pro Asn Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu		
	260	265
Asn Ile Pro Lys Tyr Ser Asn Tyr Cys Ala Asn Thr Tyr Arg Thr Gly		
	275	280
Leu Lys Asn Leu Arg Asp Glu Pro Asn Met Lys Trp Ser Ile Phe Asn		
	290	295
Asp Tyr Arg Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ser Gln		
	305	310
Phe Ser Leu Tyr Asp Ile Lys Arg Tyr Arg Asp Ser Ile Gly Gly Ile		
	325	330
Glu Val Lys Gly Ile Lys Asn Glu Leu Thr Arg Glu Ile Tyr Thr Thr		
	340	345
Glu Ile Asn Phe Asp Arg Leu Pro Gln Leu Arg Val Gln Pro Asn Leu		
	355	360
Ala Thr Met Glu Tyr Asn Leu Thr Arg Ala Ser Phe Lys Leu Phe Ser		
	370	375
Phe Leu Glu Gln Phe Ile Phe Tyr Thr Glu Asn Thr Asn Phe Gly Asn		
	385	390
Arg Leu Val Gly Ile Ser Asn Arg Asp Ala Pro Thr Tyr Ser Asn Thr		
	405	410
Ile Thr Glu Thr Leu Tyr Gly Glu Arg Thr Gly Ser Pro Thr Thr Lys		
	420	425
Thr Ile Arg Pro Phe Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg		
	435	440
Gln Ser Pro Pro Val Ser Pro Ile Gln Pro His Phe Ile Ile Asn Gln		
	450	455
Ile Glu Leu Tyr Leu Asn Gly Ser Ser Asn Asn Thr Leu Lys Tyr Ser		
	465	470
Ala Gly Gly Ser Leu Ser Asn Tyr Gln Asn Thr Thr Phe Phe Gln Phe		
	485	490
Pro Arg Lys Lys Asp Cys Asn Leu Val Ile Asp Pro Gly Cys Ser Pro		
	500	505
Asn Phe Asn Asn Tyr Ser His Ile Leu Ser His Phe Ser Leu Phe Thr		
	515	520
Tyr Ser Tyr Val Ile Gly Leu Gln Leu Gln Ile Leu Asp Thr Gly Val		
	530	535
Leu Gly Trp Thr His Ser Ser Val Asp Arg Tyr Asn Ala Ile Ser Asp		
	545	550
Lys Ile Ile Thr Met Ile Pro Ala Ile Lys Gly Asn Asn Leu Asp Thr		
	565	570
Asn Ser Lys Val Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val		
	580	585
Tyr Leu Gln Ser Gln Gly Arg Leu Glu Ile Thr Cys Glu Thr Pro Asn		
	595	600
Ser Thr Gln Ser Tyr Phe Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala		
	610	615
Gly Asn Thr Leu Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly		
	625	630
Ile Pro Pro Gln Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn		
	645	650
Asn Leu Gln Tyr Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val		
	660	665
Thr Leu Pro Leu Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp		
	675	680
Val Ser Asn Ser Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile		
	690	695
Thr Ser Ser Met His Gln Asn Arg Glu Lys Gln Lys Leu Glu Thr Ile		
	705	710
Gln Thr Lys Ile Asn Thr Phe Phe Thr Asn His Thr Lys Thr Leu		
	725	730
		735

<210> 8

<211> 2235
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> CDS
 <222> (1)...(2235)

<400> 8
 gtg aat caa aat aat aat aat gaa tat gag att atc gat tca aag aat 48
 Met Asn Gln Asn Asn Asn Glu Tyr Glu Ile Ile Asp Ser Lys Asn
 1 5 10 15
 tta tct tat cct tct aac aga aat att gat cat tct aga tac cct tac 96
 Leu Ser Tyr Pro Ser Asn Arg Asn Ile Asp His Ser Arg Tyr Pro Tyr
 20 25 30
 aca aat aat cca aat caa cca tta caa aac aca aat tac aaa gag tgg 144
 Thr Asn Asn Pro Asn Gln Pro Leu Gln Asn Thr Asn Tyr Lys Glu Trp
 35 40 45
 ctc aat atg tgt caa ggg aat aca caa tat ggt gat aat ttc gag aca 192
 Leu Asn Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu Thr
 50 55 60
 ttt gct agt gct gat aca att gct gca gtt agt gca ggt act att gta 240
 Phe Ala Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile Val
 65 70 75 80
 tcc ggt act ctg tta gcc ggt ata ggt ggg ctc act tct ata tcc gga 288
 Ser Gly Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser Gly
 85 90 95
 ccg ata gga ata ata ggt gct ata ata ata tct ttt ggt acc cta atc 336
 Pro Ile Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu Ile
 100 105 110
 act gtc ttt tgg ccc gcg gga gaa caa gac aaa aca gta tgg aca caa 384
 Thr Val Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr Gln
 115 120 125
 ttt att aaa atg gga gaa att ttt gtt gat aca ccg tta aca gaa agc 432
 Phe Ile Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu Ser
 130 135 140
 ata aaa cag cta aag tta caa act tta gaa gga ttt aga caa ata tta 480
 Ile Lys Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile Leu
 145 150 155 160
 caa agc tat aat aca gca tta gat gat tgg aga aaa tta aaa aga cta 528
 Gln Ser Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg Leu
 165 170 175
 caa gct cct gga tta cca cca tca tca gca tta caa caa gct gcc ttg 576
 Gln Ala Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala Leu
 180 185 190
 act ctt aaa ata cga ttt gag aat gtt cac aat gat ttt att cga gaa 624
 Thr Leu Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg Glu
 195 200 205
 ata cct ggt ttc caa ctt gaa act tat aaa acg cta tta cta cct att 672
 Ile Pro Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro Ile
 210 215 220
 tat gcg caa gct gct aat ttt cat tta aat tta tta caa caa ggt gct 720
 Tyr Ala Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly Ala
 225 230 235 240

gaa ttg gct gat gaa tgg aat gca gat ata cat cct tca caa att gaa	768
Glu Leu Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile Glu	
245 250 255	
cct aat gct gga aca tca gat gac tat tat aaa ctt tta aaa gaa aat	816
Pro Asn Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu Asn	
260 265 270	
ata cct aaa tat agt aac tat tgt gca aat acc tat aga gaa gga cta	864
Ile Pro Lys Tyr Ser Asn Tyr Cys Ala Asn Thr Tyr Arg Glu Gly Leu	
275 280 285	
aat aaa ctt cga aac gaa cct aat atg aga tgg agt ata ttt aat gat	912
Asn Lys Leu Arg Asn Glu Pro Asn Met Arg Trp Ser Ile Phe Asn Asp	
290 295 300	
tat cga aga tat atg act att act gta tta gat act atc gct caa ttt	960
Tyr Arg Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ala Gln Phe	
305 310 315 320	
tct ttt tat gat ata aag aga tac aaa gat tca ata gga aga ata ggt	1008
Ser Phe Tyr Asp Ile Lys Arg Tyr Lys Asp Ser Ile Gly Arg Ile Gly	
325 330 335	
ggc att aaa act gaa ctt aca aga gaa att tat aca act gaa ata aat	1056
Gly Ile Lys Thr Glu Leu Thr Arg Glu Ile Tyr Thr Thr Glu Ile Asn	
340 345 350	
ttt gac cgt ctt act tac ctt gaa att caa ccc aat ctc gct ata atg	1104
Phe Asp Arg Leu Thr Tyr Leu Glu Ile Gln Pro Asn Leu Ala Ile Met	
355 360 365	
gaa tat aat tta aca cgt tca ggg ctt aga tta ttt tca ttt tta gat	1152
Glu Tyr Asn Leu Thr Arg Ser Gly Leu Arg Leu Phe Ser Phe Leu Asp	
370 375 380	
gaa ctt ata ttt tat aca aaa aat gaa acg tac ggg aat cgt tta gtt	1200
Glu Leu Ile Phe Tyr Thr Lys Asn Glu Thr Tyr Gly Asn Arg Leu Val	
385 390 395 400	
ggg att gcg aat cgt aat aga tct act tat gct acg aca gga act gaa	1248
Gly Ile Ala Asn Arg Asn Arg Ser Thr Tyr Ala Thr Thr Gly Thr Glu	
405 410 415	
att ata tat gga gaa aga aca ggt cca ccc aca aca aaa act tta ata	1296
Ile Ile Tyr Gly Glu Arg Thr Gly Pro Pro Thr Thr Lys Thr Leu Ile	
420 425 430	
cca ttt gaa tcc tat aaa gtt tca att gta act gat aga caa gta act	1344
Pro Phe Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg Gln Val Thr	
435 440 445	
cct act tcc cct ttt cct aac ata tac ttt aca att aat caa att gaa	1392
Pro Thr Ser Pro Phe Pro Asn Ile Tyr Phe Thr Ile Asn Gln Ile Glu	
450 455 460	
ctt tat tta aat aat tca cct agt aat aaa tta aca tat tca gct ggg	1440
Leu Tyr Leu Asn Asn Ser Pro Ser Asn Lys Leu Thr Tyr Ser Ala Gly	
465 470 475 480	
ggg aat tta tct aat gat aaa aaa aca act gat ttt caa ttt cct gta	1488
Gly Asn Leu Ser Asn Asp Lys Lys Thr Thr Asp Phe Gln Phe Pro Val	
485 490 495	
aaa aaa gac tgt aaa cca att att aat cca aat tgt tta cca agc tat	1536
Lys Lys Asp Cys Lys Pro Ile Ile Asn Pro Asn Cys Leu Pro Ser Tyr	
500 505 510	


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aat agt tat agt cat att tta tcc cag ttt tct tta ttt aat tat tcc 1584
Asn Ser Tyr Ser His Ile Leu Ser Gln Phe Ser Leu Phe Asn Tyr Ser
      515                      520                      525

tat aaa att gga tta gcg cta aat ata tta tat aca ggt gca tta gga 1632
Tyr Lys Ile Gly Leu Ala Leu Asn Ile Leu Tyr Thr Gly Ala Leu Gly
      530                      535                      540

tgg aca cac agt agt gtt aat aga aat aat gca ata tca gat aaa ata 1680
Trp Thr His Ser Ser Val Asn Arg Asn Asn Ala Ile Ser Asp Lys Ile
      545                      550                      555

att aca atg atc cca gca atc aaa ggt aac agt ctt gat aca aac tct 1728
Ile Thr Met Ile Pro Ala Ile Lys Gly Asn Ser Leu Asp Thr Asn Ser
      565                      570                      575

aag gta att gaa gga cct ggt cat aca gga gga aac ttg gtt tat tta 1776
Lys Val Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val Tyr Leu
      580                      585                      590

caa agt caa ggg cgt tta gag att aca tgt aga act cct aat tct aca 1824
Gln Ser Gln Gly Arg Leu Glu Ile Thr Cys Arg Thr Pro Asn Ser Thr
      595                      600                      605

caa tct tat tac att aga ctt cga tac gct aca aat ggt gct gga aat 1872
Gln Ser Tyr Tyr Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala Gly Asn
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act ctt cct aat ata tct ctt aca ata cca gga gta ata gga ata cca 1920
Thr Leu Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly Ile Pro
      625                      630                      635                      640

cct caa cga ctc aac aac act ttt tct ggt aca aat tat aat aat tta 1968
Pro Gln Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn Asn Leu
      645                      650                      655

caa tac gga gat ttt ggg tat ttc caa ttt cca agt aca gta aca tta 2016
Gln Tyr Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val Thr Leu
      660                      665                      670

cct tta aat cga aac ata cca ttt ata ttt aat cgt gca gat gta tca 2064
Pro Leu Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp Val Ser
      675                      680                      685

aat tca att tta atc att gat aaa att gaa ttt ata cca att act tcc 2112
Asn Ser Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile Thr Ser
      690                      695                      700

tct gta cgc caa aat aga gaa aaa caa aaa tta gaa act atc caa aca 2160
Ser Val Arg Gln Asn Arg Glu Lys Gln Lys Leu Glu Thr Ile Gln Thr
      705                      710                      715                      720

aaa ata aat aca ttt ttc aca aat cat aca aaa aat act tta aat ata 2208
Lys Ile Asn Thr Phe Phe Thr Asn His Thr Lys Asn Thr Leu Asn Ile
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<213> Bacillus thuringiensis

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 Leu Asn Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu Thr
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 Phe Ala Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile Val
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 Ser Gly Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser Gly
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 Pro Ile Gly Ile Ile Gly Ala Ile Ile Ser Phe Gly Thr Leu Ile
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 Thr Val Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr Gln
 115 120 125
 Phe Ile Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu Ser
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 Asn Ser Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg Leu
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 Gln Ala Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala Leu
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 Thr Leu Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg Glu
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 Pro Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Pro Ile
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 Tyr Ala Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly Ala
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 Glu Leu Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile Glu
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 Pro Asn Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu Asn
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 Gly Ile Lys Thr Glu Leu Thr Arg Glu Ile Tyr Thr Thr Glu Ile Asn
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 Glu Tyr Asn Leu Thr Arg Ser Gly Leu Arg Leu Phe Ser Phe Leu Asp
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 Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile Val Ser Gly
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 Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser Gly Pro Ile
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 Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu Ile Thr Val
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 Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr Gln Phe Ile
 65 70 75 80
 aaa atg gga gaa att ttt gtt gat aca ccg tta aca gaa agc ata aaa 288
 Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu Ser Ile Lys
 85 90 95
 cag cta aag tta caa act tta gaa gga ttt aga caa ata tta caa agc 336
 Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile Leu Gln Ser
 100 105 110
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cct gga tta cca cca tca tca gca tta caa caa gct gcc ttg act ctt			432
Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala Leu Thr Leu			
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aaa ata cga ttt gag aat gtt cac aat gat ttt att cga gaa ata cct			480
Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg Glu Ile Pro			
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ggg ttc caa ctt gaa act tat aaa acg cta tta cta cct att tat gcg			528
Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro Ile Tyr Ala			
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caa gct gct aat ttt cat tta aat tta tta caa caa ggt gct gaa ttg			576
Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly Ala Glu Leu			
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gct gat gaa tgg aat gca gat ata cat cct tca caa att gaa cct aat			624
Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile Glu Pro Asn			
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ctt cga aac gaa cct aat atg aga tgg agt ata ttt aat gat tat cga			768
Leu Arg Asn Glu Pro Asn Met Arg Trp Ser Ile Phe Asn Asp Tyr Arg			
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aga tat atg act att act gta tta gat act atc gct caa ttt tct ttt			816
Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ala Gln Phe Ser Phe			
	260	265	270
tat gat ata aag aga tac aaa gat tca ata gga aga ata ggt ggc att			864
Tyr Asp Ile Lys Arg Tyr Lys Asp Ser Ile Gly Arg Ile Gly Gly Ile			
	275	280	285
aaa act gaa ctt aca aga gaa att tat aca act gaa ata aat ttt gac			912
Lys Thr Glu Leu Thr Arg Glu Ile Tyr Thr Thr Glu Ile Asn Phe Asp			
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Arg Leu Thr Tyr Leu Glu Ile Gln Pro Asn Leu Ala Ile Met Glu Tyr			
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Asn Leu Thr Arg Ser Gly Leu Arg Leu Phe Ser Phe Leu Asp Glu Leu			
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Ile Phe Tyr Thr Lys Asn Glu Thr Tyr Gly Asn Arg Leu Val Gly Ile			
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Ala Asn Arg Asn Arg Ser Thr Tyr Ala Thr Thr Gly Thr Glu Ile Ile			
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tat gga gaa aga aca ggt cca ccc aca aca aaa act tta ata cca ttt			1152
Tyr Gly Glu Arg Thr Gly Pro Pro Thr Thr Lys Thr Leu Ile Pro Phe			
	370	375	380
gaa tcc tat aaa gtt tca att gta act gat aga caa gta act cct act			1200
Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg Gln Val Thr Pro Thr			

385	390	395	400	
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Ser Pro Phe Pro Asn Ile Tyr Phe Thr Ile Asn Gln Ile Glu Leu Tyr	405	410	415	
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Leu Asn Asn Ser Pro Ser Asn Lys Leu Thr Tyr Ser Ala Gly Gly Asn	420	425	430	
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Leu Ser Asn Asp Lys Lys Thr Thr Asp Phe Gln Phe Pro Val Lys Lys	435	440	445	
gac tgt aaa cca att att aat cca aat tgt tta cca agc tat aat agt				1392
Asp Cys Lys Pro Ile Ile Asn Pro Asn Cys Leu Pro Ser Tyr Asn Ser	450	455	460	
tat agt cat att tta tcc cag ttt tct tta ttt aat tat tcc tat aaa				1440
Tyr Ser His Ile Leu Ser Gln Phe Ser Leu Phe Asn Tyr Ser Tyr Lys	465	470	475	480
att gga tta gcg cta aat ata tta tat aca ggt gca tta gga tgg aca				1488
Ile Gly Leu Ala Leu Asn Ile Leu Tyr Thr Gly Ala Leu Gly Trp Thr	485	490	495	
cac agt agt gtt aat aga aat aat gca ata tca gat aaa ata att aca				1536
His Ser Ser Val Asn Arg Asn Asn Ala Ile Ser Asp Lys Ile Ile Thr	500	505	510	
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Met Ile Pro Ala Ile Lys Gly Asn Ser Leu Asp Thr Asn Ser Lys Val	515	520	525	
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Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val Tyr Leu Gln Ser	530	535	540	
caa ggg cgt tta gag att aca tgt aga act cct aat tct aca caa tct				1680
Gln Gly Arg Leu Glu Ile Thr Cys Arg Thr Pro Asn Ser Thr Gln Ser	545	550	555	560
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Tyr Tyr Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala Gly Asn Thr Leu	565	570	575	
cct aat ata tct ctt aca ata cca gga gta ata gga ata cca cct caa				1776
Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly Ile Pro Pro Gln	580	585	590	
cga ctc aac aac act ttt tct ggt aca aat tat aat aat tta caa tac				1824
Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn Asn Leu Gln Tyr	595	600	605	
gga gat ttt ggg tat ttc caa ttt cca agt aca gta aca tta cct tta				1872
Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val Thr Leu Pro Leu	610	615	620	
aat cga aac ata cca ttt ata ttt aat cgt gca gat gta tca aat tca				1920
Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp Val Ser Asn Ser	625	630	635	640
att tta atc att gat aaa att gaa ttt ata cca att act tcc tct gta				1968
Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile Thr Ser Ser Val	645	650	655	
cgc caa aat aga gaa aaa caa aaa tta gaa act atc caa aca aaa ata				2016
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 Tyr Ser His Ile Leu Ser Gln Phe Ser Leu Phe Asn Tyr Ser Tyr Lys
 465 470 475 480
 Ile Gly Leu Ala Leu Asn Ile Leu Tyr Thr Gly Ala Leu Gly Trp Thr
 485 490 495
 His Ser Ser Val Asn Arg Asn Asn Ala Ile Ser Asp Lys Ile Ile Thr
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gttttcccag ttccaggaga tccaagtaat aaaagatttt gtttcccttc aaaaaatcgc 4740
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taattcttga gccattttta ctctcgaaat ttgcgtttct tgattaagtt tgctactttt 4860
ttcgtttgac gagattcaat ctctatattg aaaatatcac gcagaaattg ttctttggtt 4920
tcaaaaggta tttcatcata atggtctata atatatgctta aatgcagtga tttacaggcg 4980
tcttgcaagt ttcgttgatc cataatgaga atgaacccct ttctaaagt ggacaaagc 5040
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cttgccattt ttgtggatc gtcacttggt gagtctgcaa tatgatatcg agttcgtgag 5160
gagctttttt caaccattct tcattctcta acagtaagtg tagctgctgt aatgagttat 5220
tttgaaattaa atatttgaat cctgttaaac aagcttttct ttcactctta tgaaagagca 5280
gataatcttg aaccgcgtga ggtaaatatt tgaaaaatct agaataacga acaacgcgtg 5340
gtttcttttc ccaatcttca aaaatctctt cccatagaat cggcctactc gtgtgcatat 5400
acggctctgta ttctgtaaaa atgttctcgc cttctgcggg ataacatgta aattgatccc 5460

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attctttttt aatgataatc acttggttta cgtaaaacaa aacgttcttg atccactgtg 5520
atttctccat atttatttac cgttggtgtg tccattgaga agaccgttag gtcttccaaa 5580
ggtaaatggt tcaatgcagc cttatcatca ttccaaaggt cttcaatcat gacttccttc 5640
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gaaaaactct ccataatcgg agcgggttga aaccaattgt ttcgtgtata actgactttc 5760
cggttaacgt tcccccttcc atgcccgcta taaggattac aagggttgac ttcaaagtta 5820
taatgcattt gaaattgtaa aaatgcattc gtataagttc gattatcacc ttttctact 5880
gtgactacag cggcagataa gttatcaatt cgaagatgcg ttggtacacc accagcttga 5940
tgaaataatc gttttaagcc ttctaaaaag cttctgtat 5980

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<210> 13
 <211> 2082
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> CDS
 <222> (1)... (2082)

<400> 13
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 1 5 10 15
 gaa tcc tca tgc aat aac aca aat acg cca aac aga tat cct ttt gca 96
 Glu Ser Ser Ser Asn Asn Thr Asn Thr Pro Asn Arg Tyr Pro Phe Ala
 20 25 30
 aat aat cgg gat atg tct act atg tct tgg aat gat tgt cag gga atc 144
 Asn Asn Arg Asp Met Ser Thr Met Ser Trp Asn Asp Cys Gln Gly Ile
 35 40 45
 tca tgg gat gaa att tgg gaa tca gtc gaa acg ata aca agt att ggg 192
 Ser Trp Asp Glu Ile Trp Glu Ser Val Glu Thr Ile Thr Ser Ile Gly
 50 55 60
 ata aat ctt ata gag ttt gtg ata gaa cct agt ttg ggt gga att aat 240
 Ile Asn Leu Ile Glu Phe Val Ile Glu Pro Ser Leu Gly Gly Ile Asn
 65 70 75 80
 aca cta tta tca ata ata gga aaa cta att ccg act aat cgt caa act 288
 Thr Leu Leu Ser Ile Ile Gly Lys Leu Ile Pro Thr Asn Arg Gln Thr
 85 90 95
 gtg tca gca ctt tct ata tgt gat tta tta tct ata att cgt aaa gag 336
 Val Ser Ala Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu
 100 105 110
 gta gcc gat agt gtt tta agt gat gcg att gca gat ttt gac ggt aaa 384
 Val Ala Asp Ser Val Leu Ser Asp Ala Ile Ala Asp Phe Asp Gly Lys
 115 120 125
 ttg aaa aat tat aga gag tat tat ctt tct tat ctt ggg gct tgg ctt 432
 Leu Lys Asn Tyr Arg Glu Tyr Tyr Leu Ser Tyr Leu Gly Ala Trp Leu
 130 135 140
 aaa gac ggt aaa cca ctt caa aag aca aat aat tct gat atc gga caa 480
 Lys Asp Gly Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln
 145 150 155 160
 tta gtt tat tat ttt aaa ctt tca gaa aga gat ttc aat gaa att cta 528
 Leu Val Tyr Tyr Phe Lys Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu
 165 170 175
 gga ggg tca ttg tca aga aac aat gct caa gta ttg tta tta cct act 576
 Gly Gly Ser Leu Ser Arg Asn Asn Ala Gln Val Leu Leu Leu Pro Thr

180	185	190	
ttt gca caa gct gca aat gtg cag tta tta cta tta agg gat gca gtt Phe Ala Gln Ala Ala Asn Val Gln Leu Leu Leu Leu Arg Asp Ala Val 195 200 205			624
caa tat aaa gca caa tgg ttc cca ttt ttg agt gca gag aat gta aga Gln Tyr Lys Ala Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg 210 215 220			672
tcg gaa tta ata tca cct aac agt ggt tgt gat ttt acc ggt gat tac Ser Glu Leu Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr 225 230 235 240			720
tat gag cga tta aaa tgc aaa acg gca gag tat acc aat tat tgt tta Tyr Glu Arg Leu Lys Cys Lys Thr Ala Glu Tyr Thr Asn Tyr Cys Leu 245 250 255			768
tat tgg tat cag gta ggt tta aat cag ata aaa cag ggg ggg aca ggt Tyr Trp Tyr Gln Val Gly Leu Asn Gln Ile Lys Gln Gly Gly Thr Gly 260 265 270			816
gct gac act tgg tcg aaa ttt aat aaa ttt cgt aga gaa atg acg ttg Ala Asp Thr Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu 275 280 285			864
gcg gta ttg gat att atc gct ata ttt cca act tat gat ttt gag aaa Ala Val Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys 290 295 300			912
tat cca ttg cca aca cat gta gag ttg act agg gaa att tat aca gat Tyr Pro Leu Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp 305 310 315 320			960
gca gtg gga tat tca tcg gga act tat agt tgg tta cgg aat tgg cct Ala Val Gly Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Arg Asn Trp Pro 325 330 335			1008
aat act ttt aat ggg tta gag gct aat gga aca cgg gga cct ggt tta Asn Thr Phe Asn Gly Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu 340 345 350			1056
gtt act tgg ctt agc aaa ata ggt ata tat aat gag tat gtt tcg aga Val Thr Trp Leu Ser Lys Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg 355 360 365			1104
tat ttt gcc ggc tgg gta gga act cgt cat tat gaa gac tac aca aag Tyr Phe Ala Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Lys 370 375 380			1152
ggt aac ggt att ttt caa cgt atg tct gga act acg agt aat gat cta Gly Asn Gly Ile Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu 385 390 395 400			1200
cgt aat att gat ttt cag aat gcc gat gta tat aaa att act tca tta Arg Asn Ile Asp Phe Gln Asn Ala Asp Val Tyr Lys Ile Thr Ser Leu 405 410 415			1248
gct atc atg aac cta gta gga gag act acc gct aga cca gag tat cgt Ala Ile Met Asn Leu Val Gly Glu Thr Thr Ala Arg Pro Glu Tyr Arg 420 425 430			1296
gtt tca aag gca gat ttt cgt agg gta ggg gga cct gat tta aat tat Val Ser Lys Ala Asp Phe Arg Arg Val Gly Gly Pro Asp Leu Asn Tyr 435 440 445			1344
gat gca ggt aat aat ggg cta agc agg atg aca att gaa tct acg ttc Asp Ala Gly Asn Asn Gly Leu Ser Arg Met Thr Ile Glu Ser Thr Phe 450 455 460			1392

450	455	460	
cca ctt gta ttg cac tct aat ggt gtt aga gga ccc tct cat aga tta			1440
Pro Leu Val Leu His Ser Asn Gly Val Arg Gly Pro Ser His Arg Leu			
465	470	475	480
tca aat gcg gca tgt gtt gta tat gga aac tcc aga gtt aac gta tat			1488
Ser Asn Ala Ala Cys Val Val Tyr Gly Asn Ser Arg Val Asn Val Tyr			
	485	490	495
ggg tgg aca cat aca agt tta aaa cgt gaa aat ata att gaa gcc aat			1536
Gly Trp Thr His Thr Ser Leu Lys Arg Glu Asn Ile Ile Glu Ala Asn			
	500	505	510
caa att aca caa ata ccg gcg gtg aag agt tat tac ctt caa aat tat			1584
Gln Ile Thr Gln Ile Pro Ala Val Lys Ser Tyr Tyr Leu Gln Asn Tyr			
	515	520	525
ctt gct aat gcc tat acc tat gta ata aaa ggc act cat aca ggt ggg			1632
Leu Ala Asn Ala Tyr Thr Tyr Val Ile Lys Gly Thr His Thr Gly Gly			
	530	535	540
gat tta atc cgt ttt tta aga aca aaa tca gag tat aac gca gtt tat			1680
Asp Leu Ile Arg Phe Leu Arg Thr Lys Ser Glu Tyr Asn Ala Val Tyr			
	545	550	555
gca ggt ggc gga att aga ttg att att aat aac aaa act gca gga caa			1728
Ala Gly Gly Gly Ile Arg Leu Ile Ile Asn Asn Lys Thr Ala Gly Gln			
	565	570	575
agt tac cgt att cgt ttt cgt tat gct gca gat aaa gct gct ttc ttt			1776
Ser Tyr Arg Ile Arg Phe Arg Tyr Ala Ala Asp Lys Ala Ala Phe Phe			
	580	585	590
agt gta tat ctt tat cca gga ggt tgg ggt tca aat cgt ttt gta tcg			1824
Ser Val Tyr Leu Tyr Pro Gly Gly Trp Gly Ser Asn Arg Phe Val Ser			
	595	600	605
ctt gaa aaa tct tac tct gga aat tat gac gat tta aaa tat agt gat			1872
Leu Glu Lys Ser Tyr Ser Gly Asn Tyr Asp Asp Leu Lys Tyr Ser Asp			
	610	615	620
ttt aaa ttc gct gaa att atc aca cct cca tta cct agt tca aac att			1920
Phe Lys Phe Ala Glu Ile Ile Thr Pro Pro Leu Pro Ser Ser Asn Ile			
	625	630	635
cag atg gat gtg gag atg caa gcg aat agt ttt caa tca gat gta aac			1968
Gln Met Asp Val Glu Met Gln Ala Asn Ser Phe Gln Ser Asp Val Asn			
	645	650	655
gtg gtt ctc gac aaa att gaa ttc ctc cca agt aat aca aca act tta			2016
Val Val Leu Asp Lys Ile Glu Phe Leu Pro Ser Asn Thr Thr Thr Leu			
	660	665	670
gaa tat gag gga gaa cgg gac cta gaa aaa aca aag aac gcg gtg aac			2064
Glu Tyr Glu Gly Glu Arg Asp Leu Glu Lys Thr Lys Asn Ala Val Asn			
	675	680	685
gat ctg ttt acc aat taa			2082
Asp Leu Phe Thr Asn *			
690			

<210> 14

<211> 693

<212> PRT

<213> Bacillus thuringiensis

<400> 14
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Asn Asn Arg Asp Met Ser Thr Met Ser Trp Asn Asp Cys Gln Gly Ile
35 40 45
Ser Trp Asp Glu Ile Trp Glu Ser Val Glu Thr Ile Thr Ser Ile Gly
50 55 60
Ile Asn Leu Ile Glu Phe Val Ile Glu Pro Ser Leu Gly Gly Ile Asn
65 70 75 80
Thr Leu Leu Ser Ile Ile Gly Lys Leu Ile Pro Thr Asn Arg Gln Thr
85 90 95
Val Ser Ala Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu
100 105 110
Val Ala Asp Ser Val Leu Ser Asp Ala Ile Ala Asp Phe Asp Gly Lys
115 120 125
Leu Lys Asn Tyr Arg Glu Tyr Tyr Leu Ser Tyr Leu Gly Ala Trp Leu
130 135 140
Lys Asp Gly Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln
145 150 155 160
Leu Val Tyr Tyr Phe Lys Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu
165 170 175
Gly Gly Ser Leu Ser Arg Asn Asn Ala Gln Val Leu Leu Leu Pro Thr
180 185 190
Phe Ala Gln Ala Ala Asn Val Gln Leu Leu Leu Leu Arg Asp Ala Val
195 200 205
Gln Tyr Lys Ala Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg
210 215 220
Ser Glu Leu Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr
225 230 235 240
Tyr Glu Arg Leu Lys Cys Lys Thr Ala Glu Tyr Thr Asn Tyr Cys Leu
245 250 255
Tyr Trp Tyr Gln Val Gly Leu Asn Gln Ile Lys Gln Gly Gly Thr Gly
260 265 270
Ala Asp Thr Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu
275 280 285
Ala Val Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys
290 295 300
Tyr Pro Leu Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp
305 310 315 320
Ala Val Gly Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Arg Asn Trp Pro
325 330 335
Asn Thr Phe Asn Gly Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu
340 345 350
Val Thr Trp Leu Ser Lys Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg
355 360 365
Tyr Phe Ala Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Lys
370 375 380
Gly Asn Gly Ile Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu
385 390 395 400
Arg Asn Ile Asp Phe Gln Asn Ala Asp Val Tyr Lys Ile Thr Ser Leu
405 410 415
Ala Ile Met Asn Leu Val Gly Glu Thr Thr Ala Arg Pro Glu Tyr Arg
420 425 430
Val Ser Lys Ala Asp Phe Arg Arg Val Gly Gly Pro Asp Leu Asn Tyr
435 440 445
Asp Ala Gly Asn Asn Gly Leu Ser Arg Met Thr Ile Glu Ser Thr Phe
450 455 460
Pro Leu Val Leu His Ser Asn Gly Val Arg Gly Pro Ser His Arg Leu
465 470 475 480
Ser Asn Ala Ala Cys Val Val Tyr Gly Asn Ser Arg Val Asn Val Tyr
485 490 495
Gly Trp Thr His Thr Ser Leu Lys Arg Glu Asn Ile Ile Glu Ala Asn
500 505 510
Gln Ile Thr Gln Ile Pro Ala Val Lys Ser Tyr Tyr Leu Gln Asn Tyr
515 520 525
Leu Ala Asn Ala Tyr Thr Tyr Val Ile Lys Gly Thr His Thr Gly Gly

530 535 540
 Asp Leu Ile Arg Phe Leu Arg Thr Lys Ser Glu Tyr Asn Ala Val Tyr
 545 550 555 560
 Ala Gly Gly Gly Ile Arg Leu Ile Ile Asn Asn Lys Thr Ala Gly Gln
 565 570 575
 Ser Tyr Arg Ile Arg Phe Arg Tyr Ala Ala Asp Lys Ala Ala Phe Phe
 580 585 590
 Ser Val Tyr Leu Tyr Pro Gly Gly Trp Gly Ser Asn Arg Phe Val Ser
 595 600 605
 Leu Glu Lys Ser Tyr Ser Gly Asn Tyr Asp Asp Leu Lys Tyr Ser Asp
 610 615 620
 Phe Lys Phe Ala Glu Ile Ile Thr Pro Pro Leu Pro Ser Ser Asn Ile
 625 630 635 640
 Gln Met Asp Val Glu Met Gln Ala Asn Ser Phe Gln Ser Asp Val Asn
 645 650 655
 Val Val Leu Asp Lys Ile Glu Phe Leu Pro Ser Asn Thr Thr Thr Leu
 660 665 670
 Glu Tyr Glu Gly Glu Arg Asp Leu Glu Lys Thr Lys Asn Ala Val Asn
 675 680 685
 Asp Leu Phe Thr Asn
 690

<210> 15
 <211> 2073
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> CDS
 <222> (1)...(2073)

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 1 5 10 15
 tcg aat aac aca aat acg cca aac aga tat cct ttt gca aat aat cgg 96
 Ser Asn Asn Thr Asn Thr Pro Asn Arg Tyr Pro Phe Ala Asn Asn Arg
 20 25 30
 gat atg tct act atg tct tgg aat gat tgt cag gga atc tca tgg gat 144
 Asp Met Ser Thr Met Ser Trp Asn Asp Cys Gln Gly Ile Ser Trp Asp
 35 40 45
 gaa att tgg gaa tca gtc gaa acg ata aca agt att ggg ata aat ctt 192
 Glu Ile Trp Glu Ser Val Glu Thr Ile Thr Ser Ile Gly Ile Asn Leu
 50 55 60
 ata gag ttt gtg ata gaa cct agt ttg ggt gga att aat aca cta tta 240
 Ile Glu Phe Val Ile Glu Pro Ser Leu Gly Gly Ile Asn Thr Leu Leu
 65 70 75 80
 tca ata ata gga aaa cta att ccg act aat cgt caa act gtg tca gca 288
 Ser Ile Ile Gly Lys Leu Ile Pro Thr Asn Arg Gln Thr Val Ser Ala
 85 90 95
 ctt tct ata tgt gat tta tta tct ata att cgt aaa gag gta gcc gat 336
 Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu Val Ala Asp
 100 105 110
 agt gtt tta agt gat gcg att gca gat ttt gac ggt aaa ttg aaa aat 384
 Ser Val Leu Ser Asp Ala Ile Ala Asp Phe Asp Gly Lys Leu Lys Asn
 115 120 125
 tat aga gag tat tat ctt tct tat ctt ggg gct tgg ctt aaa gac ggt 432
 Tyr Arg Glu Tyr Tyr Leu Ser Tyr Leu Gly Ala Trp Leu Lys Asp Gly
 130 135 140

aaa cca ctt caa aag aca aat aat tct gat atc gga caa tta gtt tat	480
Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln Leu Val Tyr	
145 150 155 160	
tat ttt aaa ctt tca gaa aga gat ttc aat gaa att cta gga ggg tca	528
Tyr Phe Lys Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu Gly Gly Ser	
165 170 175	
ttg tca aga aac aat gct caa gta ttg tta tta cct act ttt gca caa	576
Leu Ser Arg Asn Asn Ala Gln Val Leu Leu Leu Pro Thr Phe Ala Gln	
180 185 190	
gct gca aat gtg cag tta tta cta tta agg gat gca gtt caa tat aaa	624
Ala Ala Asn Val Gln Leu Leu Leu Leu Arg Asp Ala Val Gln Tyr Lys	
195 200 205	
gca caa tgg ttc cca ttt ttg agt gca gag aat gta aga tcg gaa tta	672
Ala Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg Ser Glu Leu	
210 215 220	
ata tca cct aac agt ggt tgt gat ttt acc ggt gat tac tat gag cga	720
Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr Tyr Glu Arg	
225 230 235 240	
tta aaa tgc aaa acg gca gag tat acc aat tat tgt tta tat tgg tat	768
Leu Lys Cys Lys Thr Ala Glu Tyr Thr Asn Tyr Cys Leu Tyr Trp Tyr	
245 250 255	
cag gta ggt tta aat cag ata aaa cag ggg ggg aca ggt gct gac act	816
Gln Val Gly Leu Asn Gln Ile Lys Gln Gly Gly Thr Gly Ala Asp Thr	
260 265 270	
tgg tcg aaa ttt aat aaa ttt cgt aga gaa atg acg ttg gcg gta ttg	864
Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Ala Val Leu	
275 280 285	
gat att atc gct ata ttt cca act tat gat ttt gag aaa tat cca ttg	912
Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys Tyr Pro Leu	
290 295 300	
cca aca cat gta gag ttg act agg gaa att tat aca gat gca gtg gga	960
Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Ala Val Gly	
305 310 315 320	
tat tca tcg gga act tat agt tgg tta cgg aat tgg cct aat act ttt	1008
Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Arg Asn Trp Pro Asn Thr Phe	
325 330 335	
aat ggg tta gag gct aat gga aca cgg gga cct ggt tta gtt act tgg	1056
Asn Gly Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp	
340 345 350	
ctt agc aaa ata ggt ata tat aat gag tat gtt tcg aga tat ttt gcc	1104
Leu Ser Lys Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg Tyr Phe Ala	
355 360 365	
ggc tgg gta gga act cgt cat tat gaa gac tac aca aag ggt aac ggt	1152
Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Lys Gly Asn Gly	
370 375 380	
att ttt caa cgt atg tct gga act acg agt aat gat cta cgt aat att	1200
Ile Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu Arg Asn Ile	
385 390 395 400	
gat ttt cag aat gcc gat gta tat aaa att act tca tta gct atc atg	1248
Asp Phe Gln Asn Ala Asp Val Tyr Lys Ile Thr Ser Leu Ala Ile Met	
405 410 415	

aac cta gta gga gag act acc gct aga cca gag tat cgt gtt tca aag	1296
Asn Leu Val Gly Glu Thr Thr Ala Arg Pro Glu Tyr Arg Val Ser Lys	
420 425 430	
gca gat ttt cgt agg gta ggg gga cct gat tta aat tat gat gca ggt	1344
Ala Asp Phe Arg Arg Val Gly Gly Pro Asp Leu Asn Tyr Asp Ala Gly	
435 440 445	
aat aat ggg cta agc agg atg aca att gaa tct acg ttc cca ctt gta	1392
Asn Asn Gly Leu Ser Arg Met Thr Ile Glu Ser Thr Phe Pro Leu Val	
450 455 460	
ttg cac tct aat ggt gtt aga gga ccc tct cat aga tta tca aat gcg	1440
Leu His Ser Asn Gly Val Arg Gly Pro Ser His Arg Leu Ser Asn Ala	
465 470 475 480	
gca tgt gtt gta tat gga aac tcc aga gtt aac gta tat ggt tgg aca	1488
Ala Cys Val Val Tyr Gly Asn Ser Arg Val Asn Val Tyr Gly Trp Thr	
485 490 495	
cat aca agt tta aaa cgt gaa aat ata att gaa gcc aat caa att aca	1536
His Thr Ser Leu Lys Arg Glu Asn Ile Ile Glu Ala Asn Gln Ile Thr	
500 505 510	
caa ata ccg gcg gtg aag agt tat tac ctt caa aat tat ctt gct aat	1584
Gln Ile Pro Ala Val Lys Ser Tyr Tyr Leu Gln Asn Tyr Leu Ala Asn	
515 520 525	
gcc tat acc tat gta ata aaa ggc act cat aca ggt ggg gat tta atc	1632
Ala Tyr Thr Tyr Val Ile Lys Gly Thr His Thr Gly Gly Asp Leu Ile	
530 535 540	
cgt ttt tta aga aca aaa tca gag tat aac gca gtt tat gca ggt ggc	1680
Arg Phe Leu Arg Thr Lys Ser Glu Tyr Asn Ala Val Tyr Ala Gly Gly	
545 550 555 560	
gga att aga ttg att att aat aac aaa act gca gga caa agt tac cgt	1728
Gly Ile Arg Leu Ile Ile Asn Asn Lys Thr Ala Gly Gln Ser Tyr Arg	
565 570 575	
att cgt ttt cgt tat gct gca gat aaa gct gct ttc ttt agt gta tat	1776
Ile Arg Phe Arg Tyr Ala Ala Asp Lys Ala Ala Phe Phe Ser Val Tyr	
580 585 590	
ctt tat cca gga ggt tgg ggt tca aat cgt ttt gta tcg ctt gaa aaa	1824
Leu Tyr Pro Gly Gly Trp Gly Ser Asn Arg Phe Val Ser Leu Glu Lys	
595 600 605	
tct tac tct gga aat tat gac gat tta aaa tat agt gat ttt aaa ttc	1872
Ser Tyr Ser Gly Asn Tyr Asp Asp Leu Lys Tyr Ser Asp Phe Lys Phe	
610 615 620	
gct gaa att atc aca cct cca tta cct agt tca aac att cag atg gat	1920
Ala Glu Ile Ile Thr Pro Leu Pro Ser Ser Asn Ile Gln Met Asp	
625 630 635 640	
gtg gag atg caa gcg aat agt ttt caa tca gat gta aac gtg gtt ctc	1968
Val Glu Met Gln Ala Asn Ser Phe Gln Ser Asp Val Asn Val Val Leu	
645 650 655	
gac aaa att gaa ttc ctc cca agt aat aca aca act tta gaa tat gag	2016
Asp Lys Ile Glu Phe Leu Pro Ser Asn Thr Thr Thr Leu Glu Tyr Glu	
660 665 670	
gga gaa cgg gac cta gaa aaa aca aag aac gcg gtg aac gat ctg ttt	2064
Gly Glu Arg Asp Leu Glu Lys Thr Lys Asn Ala Val Asn Asp Leu Phe	
675 680 685	

acc aat taa
Thr Asn *
690

2073

<210> 16
<211> 690
<212> PRT
<213> Bacillus thuringiensis

<400> 16
Met Ser Pro Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Leu Glu Ser Ser
1 5 10 15
Ser Asn Asn Thr Asn Thr Pro Asn Arg Tyr Pro Phe Ala Asn Asn Arg
20 25 30
Asp Met Ser Thr Met Ser Trp Asn Asp Cys Gln Gly Ile Ser Trp Asp
35 40 45
Glu Ile Trp Glu Ser Val Glu Thr Ile Thr Ser Ile Gly Ile Asn Leu
50 55 60
Ile Glu Phe Val Ile Glu Pro Ser Leu Gly Gly Ile Asn Thr Leu Leu
65 70 75 80
Ser Ile Ile Gly Lys Leu Ile Pro Thr Asn Arg Gln Thr Val Ser Ala
85 90 95
Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu Val Ala Asp
100 105 110
Ser Val Leu Ser Asp Ala Ile Ala Asp Phe Asp Gly Lys Leu Lys Asn
115 120 125
Tyr Arg Glu Tyr Tyr Leu Ser Tyr Leu Gly Ala Trp Leu Lys Asp Gly
130 135 140
Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln Leu Val Tyr
145 150 155 160
Tyr Phe Lys Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu Gly Gly Ser
165 170 175
Leu Ser Arg Asn Asn Ala Gln Val Leu Leu Leu Pro Thr Phe Ala Gln
180 185 190
Ala Ala Asn Val Gln Leu Leu Leu Arg Asp Ala Val Gln Tyr Lys
195 200 205
Ala Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg Ser Glu Leu
210 215 220
Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr Tyr Glu Arg
225 230 235 240
Leu Lys Cys Lys Thr Ala Glu Tyr Thr Asn Tyr Cys Leu Tyr Trp Tyr
245 250 255
Gln Val Gly Leu Asn Gln Ile Lys Gln Gly Gly Thr Gly Ala Asp Thr
260 265 270
Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Ala Val Leu
275 280 285
Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys Tyr Pro Leu
290 295 300
Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Ala Val Gly
305 310 315 320
Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Arg Asn Trp Pro Asn Thr Phe
325 330 335
Asn Gly Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp
340 345 350
Leu Ser Lys Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg Tyr Phe Ala
355 360 365
Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Lys Gly Asn Gly
370 375 380
Ile Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu Arg Asn Ile
385 390 395 400
Asp Phe Gln Asn Ala Asp Val Tyr Lys Ile Thr Ser Leu Ala Ile Met
405 410 415
Asn Leu Val Gly Glu Thr Thr Ala Arg Pro Glu Tyr Arg Val Ser Lys
420 425 430
Ala Asp Phe Arg Arg Val Gly Gly Pro Asp Leu Asn Tyr Asp Ala Gly
435 440 445

Asn Asn Gly Leu Ser Arg Met Thr Ile Glu Ser Thr Phe Pro Leu Val
 450 455 460
 Leu His Ser Asn Gly Val Arg Gly Pro Ser His Arg Leu Ser Asn Ala
 465 470 475 480
 Ala Cys Val Val Tyr Gly Asn Ser Arg Val Asn Val Tyr Gly Trp Thr
 485 490 495
 His Thr Ser Leu Lys Arg Glu Asn Ile Ile Glu Ala Asn Gln Ile Thr
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 Gln Ile Pro Ala Val Lys Ser Tyr Tyr Leu Gln Asn Tyr Leu Ala Asn
 515 520 525
 Ala Tyr Thr Tyr Val Ile Lys Gly Thr His Thr Gly Gly Asp Leu Ile
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 Arg Phe Leu Arg Thr Lys Ser Glu Tyr Asn Ala Val Tyr Ala Gly Gly
 545 550 555 560
 Gly Ile Arg Leu Ile Ile Asn Asn Lys Thr Ala Gly Gln Ser Tyr Arg
 565 570 575
 Ile Arg Phe Arg Tyr Ala Ala Asp Lys Ala Ala Phe Phe Ser Val Tyr
 580 585 590
 Leu Tyr Pro Gly Gly Trp Gly Ser Asn Arg Phe Val Ser Leu Glu Lys
 595 600 605
 Ser Tyr Ser Gly Asn Tyr Asp Asp Leu Lys Tyr Ser Asp Phe Lys Phe
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 Ala Glu Ile Ile Thr Pro Pro Leu Pro Ser Ser Asn Ile Gln Met Asp
 625 630 635 640
 Val Glu Met Gln Ala Asn Ser Phe Gln Ser Asp Val Asn Val Val Leu
 645 650 655
 Asp Lys Ile Glu Phe Leu Pro Ser Asn Thr Thr Thr Leu Glu Tyr Glu
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 Thr Asn
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<210> 17

<211> 1686

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)...(1686)

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 Thr Thr Asp Tyr Glu Ile Asp Gln Ala Ala Ile Ser Ile Glu Cys Met
 20 25 30
 tca gat gaa caa aat cct cag gaa aaa ata atg tta tgg gat gaa ata 144
 Ser Asp Glu Gln Asn Pro Gln Glu Lys Ile Met Leu Trp Asp Glu Ile
 35 40 45
 aaa ctg gca aaa caa ctt agt cag tct cgt aat cta ctc caa aat gga 192
 Lys Leu Ala Lys Gln Leu Ser Gln Ser Arg Asn Leu Leu Gln Asn Gly
 50 55 60
 gac ttt tct ggg aat gat tgg aca ttc ggt aat gat att atc ata gga 240
 Asp Phe Ser Gly Asn Asp Trp Thr Phe Gly Asn Asp Ile Ile Ile Gly
 65 70 75 80
 tcc aat aat cct att ttt aaa gga aaa ttt cta cag atg cgt gga gca 288
 Ser Asn Asn Pro Ile Phe Lys Gly Lys Phe Leu Gln Met Arg Gly Ala
 85 90 95

cga gac ata tat gga act cta ttt cca acc tat atc tgt caa aaa ata 336
 Arg Asp Ile Tyr Gly Thr Leu Phe Pro Thr Tyr Ile Cys Gln Lys Ile
 100 105 110

gat gag tct aaa tta aaa cca tat aca cgt tat cga gta aga ggg ttt 384
 Asp Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Arg Val Arg Gly Phe
 115 120 125

gtg gga agt agt aaa gat ttg aaa tta atg gta aca cgt tac ggg aaa 432
 Val Gly Ser Ser Lys Asp Leu Lys Leu Met Val Thr Arg Tyr Gly Lys
 130 135 140

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 Glu Ile Asp Ala Ile Met Asn Val Pro Asn Asp Leu Ala Tyr Met Gln
 145 150 155 160

cct aat cct tca tgt gga gat tat cgc tgt gaa tca tcg tct cag tat 528
 Pro Asn Pro Ser Cys Gly Asp Tyr Arg Cys Glu Ser Ser Ser Gln Tyr
 165 170 175

gtg agc caa ggg tat cct aca cca aca gat gga tat gct ccc gat atg 576
 Val Ser Gln Gly Tyr Pro Thr Pro Thr Asp Gly Tyr Ala Pro Asp Met
 180 185 190

tat gca tgc ccg caa aat ata gat aga aag cat gtg aag tgt cac gat 624
 Tyr Ala Cys Pro Gln Asn Ile Asp Arg Lys His Val Lys Cys His Asp
 195 200 205

cgt cat cca ttt gat ttt cat att gac acc gga gaa gta gat aca aat 672
 Arg His Pro Phe Asp Phe His Ile Asp Thr Gly Glu Val Asp Thr Asn
 210 215 220

aca aat gta ggt att gat gtc tta tta aaa att tct aat cca gat gga 720
 Thr Asn Val Gly Ile Asp Val Leu Leu Lys Ile Ser Asn Pro Asp Gly
 225 230 235 240

tac gct aca gta ggg aat cta gaa gtc att gaa gaa gga cca cta aca 768
 Tyr Ala Thr Val Gly Asn Leu Glu Val Ile Glu Glu Gly Pro Leu Thr
 245 250 255

ggt gaa gca ttg gca cat gtg aaa caa aag gaa aag aaa tgg aaa caa 816
 Gly Glu Ala Leu Ala His Val Lys Gln Lys Glu Lys Lys Trp Lys Gln
 260 265 270

cac atg gag aaa aaa cgt tgg gaa aca caa caa gcc tat gat cca gca 864
 His Met Glu Lys Lys Arg Trp Glu Thr Gln Gln Ala Tyr Asp Pro Ala
 275 280 285

aaa cag gct gta gat gca tta ttt aca aat gaa caa gag tta cac tat 912
 Lys Gln Ala Val Asp Ala Leu Phe Thr Asn Glu Gln Glu Leu His Tyr
 290 295 300

cat att act tta gat cat att caa aac gct gat cga ctg gta cag tcg 960
 His Ile Thr Leu Asp His Ile Gln Asn Ala Asp Arg Leu Val Gln Ser
 305 310 315 320

att ccc tat gta tac cat aat tgg tta ccg aat gct cca ggt atg aac 1008
 Ile Pro Tyr Val Tyr His Asn Trp Leu Pro Asn Ala Pro Gly Met Asn
 325 330 335

tat gat gta tat caa gag tta aac gca cgt atc atg caa ggt tat aat 1056
 Tyr Asp Val Tyr Gln Glu Leu Asn Ala Arg Ile Met Gln Gly Tyr Asn
 340 345 350

tta tat gat gca cga aat gtc ata aca aat ggt gac ttt aca caa gga 1104
 Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp Phe Thr Gln Gly
 355 360 365

tta cag gga tgg cac gca aca gga aat gcc gcg gta caa caa atg gat 1152
 Leu Gln Gly Trp His Ala Thr Gly Asn Ala Ala Val Gln Gln Met Asp
 370 375 380
 gga gct tca gta tta gtt cta tca aat tgg agc gcg ggg gta tct caa 1200
 Gly Ala Ser Val Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln
 385 390 395 400
 aac ttg cat gct caa gat cat cat gga tat gtg tta cgt gtg att gcc 1248
 Asn Leu His Ala Gln Asp His His Gly Tyr Val Leu Arg Val Ile Ala
 405 410 415
 aaa aaa gaa gga cct gga aaa ggg tat gta acg atg atg gat tgt aat 1296
 Lys Lys Glu Gly Pro Gly Lys Gly Tyr Val Thr Met Met Asp Cys Asn
 420 425 430
 gga aag cag gaa aca ctt aag ttc act tct tgc gaa gaa gga tat atg 1344
 Gly Lys Glu Thr Leu Lys Phe Thr Ser Cys Glu Glu Gly Tyr Met
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 aca aaa aca gta gag gta ttc cca gaa agt gat cgt gta cgg att gaa 1392
 Thr Lys Thr Val Glu Val Phe Pro Glu Ser Asp Arg Val Arg Ile Glu
 450 455 460
 ata gga gaa acc gaa ggt aca ttt tat ata gat agc atc gag ttg ctt 1440
 Ile Gly Glu Thr Glu Gly Thr Phe Tyr Ile Asp Ser Ile Glu Leu Leu
 465 470 475 480
 tgt atg caa gga tat gat aac aat aat aac ctg cac acg ggt aat atg 1488
 Cys Met Gln Gly Tyr Asp Asn Asn Asn Asn Leu His Thr Gly Asn Met
 485 490 495
 tat gag caa agt tat aat gga aat tat aat caa aat act agc gat gtg 1536
 Tyr Glu Gln Ser Tyr Asn Gly Asn Tyr Asn Gln Asn Thr Ser Asp Val
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 Tyr Tyr Gln Gly Tyr Thr Asn Asn Tyr Asn Gln Asp Ser Ser Asn Met
 515 520 525
 tat aat caa aat tat act aac aat gat gac ctg cat tcc ggt tgc aca 1632
 Tyr Asn Gln Asn Tyr Thr Asn Asn Asp Asp Leu His Ser Gly Cys Thr
 530 535 540
 tgt aac caa ggg cat aac tct ggc tgt aca tgt aat caa gga tat aac 1680
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 cgt taa 1686
 Arg *

<210> 18
 <211> 561
 <212> PRT
 <213> Bacillus thuringiensis

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 35 40 45
 Lys Leu Ala Lys Gln Leu Ser Gln Ser Arg Asn Leu Leu Gln Asn Gly
 50 55 60
 Asp Phe Ser Gly Asn Asp Trp Thr Phe Gly Asn Asp Ile Ile Ile Gly

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65          70          75          80
Ser Asn Asn Pro Ile Phe Lys Gly Lys Phe Leu Gln Met Arg Gly Ala
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Arg Asp Ile Tyr Gly Thr Leu Phe Pro Thr Tyr Ile Cys Gln Lys Ile
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Asp Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Arg Val Arg Gly Phe
115        120        125
Val Gly Ser Ser Lys Asp Leu Lys Leu Met Val Thr Arg Tyr Gly Lys
130        135        140
Glu Ile Asp Ala Ile Met Asn Val Pro Asn Asp Leu Ala Tyr Met Gln
145        150        155        160
Pro Asn Pro Ser Cys Gly Asp Tyr Arg Cys Glu Ser Ser Ser Gln Tyr
165        170        175
Val Ser Gln Gly Tyr Pro Thr Pro Thr Asp Gly Tyr Ala Pro Asp Met
180        185        190
Tyr Ala Cys Pro Gln Asn Ile Asp Arg Lys His Val Lys Cys His Asp
195        200        205
Arg His Pro Phe Asp Phe His Ile Asp Thr Gly Glu Val Asp Thr Asn
210        215        220
Thr Asn Val Gly Ile Asp Val Leu Leu Lys Ile Ser Asn Pro Asp Gly
225        230        235        240
Tyr Ala Thr Val Gly Asn Leu Glu Val Ile Glu Glu Gly Pro Leu Thr
245        250        255
Gly Glu Ala Leu Ala His Val Lys Gln Lys Glu Lys Lys Trp Lys Gln
260        265        270
His Met Glu Lys Lys Arg Trp Glu Thr Gln Gln Ala Tyr Asp Pro Ala
275        280        285
Lys Gln Ala Val Asp Ala Leu Phe Thr Asn Glu Gln Glu Leu His Tyr
290        295        300
His Ile Thr Leu Asp His Ile Gln Asn Ala Asp Arg Leu Val Gln Ser
305        310        315        320
Ile Pro Tyr Val Tyr His Asn Trp Leu Pro Asn Ala Pro Gly Met Asn
325        330        335
Tyr Asp Val Tyr Gln Glu Leu Asn Ala Arg Ile Met Gln Gly Tyr Asn
340        345        350
Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp Phe Thr Gln Gly
355        360        365
Leu Gln Gly Trp His Ala Thr Gly Asn Ala Ala Val Gln Gln Met Asp
370        375        380
Gly Ala Ser Val Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln
385        390        395        400
Asn Leu His Ala Gln Asp His His Gly Tyr Val Leu Arg Val Ile Ala
405        410        415
Lys Lys Glu Gly Pro Gly Lys Gly Tyr Val Thr Met Met Asp Cys Asn
420        425        430
Gly Lys Gln Glu Thr Leu Lys Phe Thr Ser Cys Glu Glu Gly Tyr Met
435        440        445
Thr Lys Thr Val Glu Val Phe Pro Glu Ser Asp Arg Val Arg Ile Glu
450        455        460
Ile Gly Glu Thr Glu Gly Thr Phe Tyr Ile Asp Ser Ile Glu Leu Leu
465        470        475        480
Cys Met Gln Gly Tyr Asp Asn Asn Asn Asn Leu His Thr Gly Asn Met
485        490        495
Tyr Glu Gln Ser Tyr Asn Gly Asn Tyr Asn Gln Asn Thr Ser Asp Val
500        505        510
Tyr Tyr Gln Gly Tyr Thr Asn Asn Tyr Asn Gln Asp Ser Ser Asn Met
515        520        525
Tyr Asn Gln Asn Tyr Thr Asn Asn Asp Asp Leu His Ser Gly Cys Thr
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Cys Asn Gln Gly His Asn Ser Gly Cys Thr Cys Asn Gln Gly Tyr Asn
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Arg

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<210> 19
 <211> 2049
 <212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (1)...(2049)

<400> 19

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cga atc aac tct aat atg tct aat tgt tat cca agg tat cca cta gca 96
Arg Ile Asn Ser Asn Met Ser Asn Cys Tyr Pro Arg Tyr Pro Leu Ala
20 25 30

aaa gat cca caa atg act atg cga aac acg aac tat aaa gaa tgg cta 144
Lys Asp Pro Gln Met Thr Met Arg Asn Thr Asn Tyr Lys Glu Trp Leu
35 40 45

aat atg tgt gat tca aat aca caa ttt att ggt gat ata agc acg tat 192
Asn Met Cys Asp Ser Asn Thr Gln Phe Ile Gly Asp Ile Ser Thr Tyr
50 55 60

tct agc cct gaa gct gct tta agt gta cga gat gct gtt tta acg ggt 240
Ser Ser Pro Glu Ala Ala Leu Ser Val Arg Asp Ala Val Leu Thr Gly
65 70 75 80

att aac agt gta ggg act ata ctt tcg aat tta ggg gtc cct ttg gca 288
Ile Asn Ser Val Gly Thr Ile Leu Ser Asn Leu Gly Val Pro Leu Ala
85 90 95

agt caa tca ttt gga ata att agt agg cta ata ggt att tta tgg gca 336
Ser Gln Ser Phe Gly Ile Ile Ser Arg Leu Ile Gly Ile Leu Trp Ala
100 105 110

ggg cct gat cca ttt gaa gca ctt atg gtt ctt gtt gaa gag ctt att 384
Gly Pro Asp Pro Phe Glu Ala Leu Met Val Leu Val Glu Glu Leu Ile
115 120 125

aag aaa agt ata gat cag cgt gta aga gaa aat gct ctt aga gag cta 432
Lys Lys Ser Ile Asp Gln Arg Val Arg Glu Asn Ala Leu Arg Glu Leu
130 135 140

gaa ggt tta cag gga att atg aga cta tat caa act aga ctg caa gca 480
Glu Gly Leu Gln Gly Ile Met Arg Leu Tyr Gln Thr Arg Leu Gln Ala
145 150 155 160

tgg cta gtt aac aag aat gat gac aat cgg agg gca cta gta acg cag 528
Trp Leu Val Asn Lys Asn Asp Asp Asn Arg Arg Ala Leu Val Thr Gln
165 170 175

tat gca att gtt gat aac ttt ttc gaa aag aat atg cca aaa ttc aag 576
Tyr Ala Ile Val Asp Asn Phe Phe Glu Lys Asn Met Pro Lys Phe Lys
180 185 190

gaa aga aac ttt gaa att tta ttg tta cca gta tat gca caa gcc gcg 624
Glu Arg Asn Phe Glu Ile Leu Leu Leu Pro Val Tyr Ala Gln Ala Ala
195 200 205

aat ttg cat tta att tta tta aga gat gct gat tat ttt gga gca cag 672
Asn Leu His Leu Ile Leu Leu Arg Asp Ala Asp Tyr Phe Gly Ala Gln
210 215 220

tgg caa tta ggt gat gat gaa att cgt gat aat tat atc aga cta caa 720
Trp Gln Leu Gly Asp Asp Glu Ile Arg Asp Asn Tyr Ile Arg Leu Gln
225 230 235 240

gga ctg att aga gaa tat aaa gat cat tgt ata aca ttc tat aac cag 768

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Gly	Leu	Ile	Arg	Glu	Tyr	Lys	Asp	His	Cys	Ile	Thr	Phe	Tyr	Asn	Gln		
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Gly	Leu	Asn	Gln	Phe	Asn	Arg	Ser	Asn	Ala	Gln	Asp	Trp	Val	Ser	Phe		
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aat	agg	ttt	cgt	aca	gat	atg	aca	tta	aca	gta	tta	gat	ctc	gca	ata	864	
Asn	Arg	Phe	Arg	Thr	Asp	Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ala	Ile		
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Leu	Phe	Pro	Asn	Tyr	Asp	Pro	Arg	Arg	Tyr	Pro	Leu	Ala	Val	Lys	Thr		
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tta	gaa	agt	gga	ggt	agg	act	tac	cct	tgg	tat	aat	cct	aat	aat	aca	1008	
Leu	Glu	Ser	Gly	Gly	Arg	Thr	Tyr	Pro	Trp	Tyr	Asn	Pro	Asn	Asn	Thr		
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acc	ttt	act	gct	atg	gaa	aat	aac	gca	aga	cga	cgt	cct	tct	tat	acc	1056	
Thr	Phe	Thr	Ala	Met	Glu	Asn	Asn	Ala	Arg	Arg	Arg	Pro	Ser	Tyr	Thr		
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act	tgg	ctt	aat	cgt	att	ttt	gta	tat	aca	agg	act	cta	ggt	aat	atg	1104	
Thr	Trp	Leu	Asn	Arg	Ile	Phe	Val	Tyr	Thr	Arg	Thr	Leu	Gly	Asn	Met		
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Ser	Asp	Val	Arg	Asn	Ile	Trp	Gly	Gly	His	Thr	Leu	Val	Glu	Asn	Gly		
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Asn	Asp	Gly	Ser	Glu	Ile	Thr	His	Asn	Phe	Gly	Lys	Thr	Asp	Ser	Ile		
385					390					395					400		
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Thr	Pro	Ile	Gln	Tyr	Phe	Asn	Phe	Ala	Asn	Leu	Ser	Val	Phe	Ser	Ile		
			405						410					415			
gag	tca	ctt	gct	cgt	ata	tat	tta	gga	gga	aca	gag	gct	aat	aat	tat	1296	
Glu	Ser	Leu	Ala	Arg	Ile	Tyr	Leu	Gly	Gly	Thr	Glu	Ala	Asn	Asn	Tyr		
			420					425					430				
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Ile	Thr	Ser	Gln	Tyr	Gly	Val	Ser	Arg	Val	Ile	Phe	Asn	Thr	Ser	Asn		
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Pro	Ser	Gln	Thr	Ile	Leu	Ser	Glu	Leu	Pro	Gly	Lys	Asp	Lys	Pro	Arg		
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cca	aac	gca	gga	gat	ttc	agc	cat	aga	tta	tct	tat	ata	tca	aat	ttt	1488	
Pro	Asn	Ala	Gly	Asp	Phe	Ser	His	Arg	Leu	Ser	Tyr	Ile	Ser	Asn	Phe		
				485					490					495			
gat	gca	cgg	cga	agt	agt	tca	ggc	ggt	att	gtt	agt	ctt	tta	acg	ttt	1536	
Asp	Ala	Arg	Arg	Ser	Ser	Ser	Gly	Gly	Ile	Val	Ser	Leu	Leu	Thr	Phe		
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 ttt gtc atc cca gga cct act ggg ggg aat ttg gta aaa gtc agt gat 1680
 Phe Val Ile Pro Gly Pro Thr Gly Gly Asn Leu Val Lys Val Ser Asp
 545 550 555 560
 agt tgg cat tca ctt aaa gtt caa gca cca caa aga caa aca agt tat 1728
 Ser Trp His Ser Leu Lys Val Gln Ala Pro Gln Arg Gln Thr Ser Tyr
 565 570 575
 cgt att cgt ttg cgt tat gct tgt tta gtt acc cat ggg gat gct att 1776
 Arg Ile Arg Leu Arg Tyr Ala Cys Leu Val Thr His Gly Asp Ala Ile
 580 585 590
 ttt gta gaa cac agc ggc agt agt cat ata gtt tca ttt ttt gat tgc 1824
 Phe Val Glu His Ser Gly Ser Ser His Ile Val Ser Phe Phe Asp Cys
 595 600 605
 tca aat tca tca ggt cgt cca tca aac act ctt cta gag agt gat ttt 1872
 Ser Asn Ser Ser Gly Arg Pro Ser Asn Thr Leu Leu Glu Ser Asp Phe
 610 615 620
 cgc tat att gat gtt cca ggt att ttt aca cca tca ata aat ccc tta 1920
 Arg Tyr Ile Asp Val Pro Gly Ile Phe Thr Pro Ser Ile Asn Pro Leu
 625 630 635 640
 ata aga tat aga aca caa agc ttt ggt acc cac gcg ata gac aaa ttt 1968
 Ile Arg Tyr Arg Thr Gln Ser Phe Gly Thr His Ala Ile Asp Lys Phe
 645 650 655
 gaa ttt att cca ctt aac act ttt ccg aat caa tca tta gaa aaa aga 2016
 Glu Phe Ile Pro Leu Asn Thr Phe Pro Asn Gln Ser Leu Glu Lys Arg
 660 665 670
 gaa cag gaa gta aat gat cta ttt atc aat taa 2049
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 675 680

<210> 20

<211> 682

<212> PRT

<213> Bacillus thuringiensis

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 Lys Asp Pro Gln Met Thr Met Arg Asn Thr Asn Tyr Lys Glu Trp Leu
 35 40 45
 Asn Met Cys Asp Ser Asn Thr Gln Phe Ile Gly Asp Ile Ser Thr Tyr
 50 55 60
 Ser Ser Pro Glu Ala Ala Leu Ser Val Arg Asp Ala Val Leu Thr Gly
 65 70 75 80
 Ile Asn Ser Val Gly Thr Ile Leu Ser Asn Leu Gly Val Pro Leu Ala
 85 90 95
 Ser Gln Ser Phe Gly Ile Ile Ser Arg Leu Ile Gly Ile Leu Trp Ala
 100 105 110
 Gly Pro Asp Pro Phe Glu Ala Leu Met Val Leu Val Glu Glu Leu Ile
 115 120 125
 Lys Lys Ser Ile Asp Gln Arg Val Arg Glu Asn Ala Leu Arg Glu Leu
 130 135 140

Glu Gly Leu Gln Gly Ile Met Arg Leu Tyr Gln Thr Arg Leu Gln Ala
 145 150 155 160
 Trp Leu Val Asn Lys Asn Asp Asp Asn Arg Arg Ala Leu Val Thr Gln
 165 170 175
 Tyr Ala Ile Val Asp Asn Phe Phe Glu Lys Asn Met Pro Lys Phe Lys
 180 185 190
 Glu Arg Asn Phe Glu Ile Leu Leu Leu Pro Val Tyr Ala Gln Ala Ala
 195 200 205
 Asn Leu His Leu Ile Leu Leu Arg Asp Ala Asp Tyr Phe Gly Ala Gln
 210 215 220
 Trp Gln Leu Gly Asp Asp Glu Ile Arg Asp Asn Tyr Ile Arg Leu Gln
 225 230 235 240
 Gly Leu Ile Arg Glu Tyr Lys Asp His Cys Ile Thr Phe Tyr Asn Gln
 245 250 255
 Gly Leu Asn Gln Phe Asn Arg Ser Asn Ala Gln Asp Trp Val Ser Phe
 260 265 270
 Asn Arg Phe Arg Thr Asp Met Thr Leu Thr Val Leu Asp Leu Ala Ile
 275 280 285
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 290 295 300
 Glu Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Gly Phe Thr Gly Val
 305 310 315 320
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 325 330 335
 Thr Phe Thr Ala Met Glu Asn Asn Ala Arg Arg Arg Pro Ser Tyr Thr
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 Thr Trp Leu Asn Arg Ile Phe Val Tyr Thr Arg Thr Leu Gly Asn Met
 355 360 365
 Ser Asp Val Arg Asn Ile Trp Gly Gly His Thr Leu Val Glu Asn Gly
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 Asn Asp Gly Ser Glu Ile Thr His Asn Phe Gly Lys Thr Asp Ser Ile
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 Thr Pro Ile Gln Tyr Phe Asn Phe Ala Asn Leu Ser Val Phe Ser Ile
 405 410 415
 Glu Ser Leu Ala Arg Ile Tyr Leu Gly Gly Thr Glu Ala Asn Asn Tyr
 420 425 430
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 435 440 445
 Ile Asn Asn Val Pro Gly Ser Leu Arg Tyr Glu Val Pro Ala Asn Leu
 450 455 460
 Pro Ser Gln Thr Ile Leu Ser Glu Leu Pro Gly Lys Asp Lys Pro Arg
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 Pro Asn Ala Gly Asp Phe Ser His Arg Leu Ser Tyr Ile Ser Asn Phe
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 Asp Ala Arg Arg Ser Ser Ser Gly Gly Ile Val Ser Leu Leu Thr Phe
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 Arg Tyr Pro Leu Ala Lys Asp Pro Gln Met Thr Met Arg Asn Thr Asn
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 tat aaa gaa tgg cta aat atg tgt gat tca aat aca caa ttt att ggt 144
 Tyr Lys Glu Trp Leu Asn Met Cys Asp Ser Asn Thr Gln Phe Ile Gly
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 Asp Ile Ser Thr Tyr Ser Ser Pro Glu Ala Ala Leu Ser Val Arg Asp
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 Ala Val Leu Thr Gly Ile Asn Ser Val Gly Thr Ile Leu Ser Asn Leu
 65 70 75 80
 ggg gtc cct ttg gca agt caa tca ttt gga ata att agt agg cta ata 288
 Gly Val Pro Leu Ala Ser Gln Ser Phe Gly Ile Ile Ser Arg Leu Ile
 85 90 95
 ggt att tta tgg gca ggg cct gat cca ttt gaa gca ctt atg gtt ctt 336
 Gly Ile Leu Trp Ala Gly Pro Asp Pro Phe Glu Ala Leu Met Val Leu
 100 105 110
 gtt gaa gag ctt att aag aaa agt ata gat cag cgt gta aga gaa aat 384
 Val Glu Glu Leu Ile Lys Lys Ser Ile Asp Gln Arg Val Arg Glu Asn
 115 120 125
 gct ctt aga gag cta gaa ggt tta cag gga att atg aga cta tat caa 432
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 Thr Arg Leu Gln Ala Trp Leu Val Asn Lys Asn Asp Asp Asn Arg Arg
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 Tyr Phe Gly Ala Gln Trp Gln Leu Gly Asp Asp Glu Ile Arg Asp Asn
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Tyr Ile Arg Leu Gln Gly Leu Ile Arg Glu Tyr Lys Asp His Cys Ile	
225 230 235 240	
aca ttc tat aac cag ggt tta aat caa ttt aat cgc tca aat gct caa	768
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245 250 255	
gat tgg gtg agc ttt aat agg ttt cgt aca gat atg aca tta aca gta	816
Asp Trp Val Ser Phe Asn Arg Phe Arg Thr Asp Met Thr Leu Thr Val	
260 265 270	
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275 280 285	
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Leu Ala Val Lys Thr Glu Leu Thr Arg Glu Val Tyr Thr Asp Pro Val	
290 295 300	
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Arg Pro Ser Tyr Thr Thr Trp Leu Asn Arg Ile Phe Val Tyr Thr Arg	
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Thr Leu Gly Asn Met Ser Asp Val Arg Asn Ile Trp Gly Gly His Thr	
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tta gtt gaa aat gga aat gat ggt tct gaa ata acc cat aac ttt ggt	1152
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Lys Thr Asp Ser Ile Thr Pro Ile Gln Tyr Phe Asn Phe Ala Asn Leu	
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420 425 430	
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Phe Asn Thr Ser Asn Ile Asn Asn Val Pro Gly Ser Leu Arg Tyr Glu	
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Val Pro Ala Asn Leu Pro Ser Gln Thr Ile Leu Ser Glu Leu Pro Gly	
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Lys Asp Lys Pro Arg Pro Asn Ala Gly Asp Phe Ser His Arg Leu Ser	
465 470 475 480	
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Tyr Ile Ser Asn Phe Asp Ala Arg Ser Ser Ser Gly Gly Ile Val	
485 490 495	

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Ser Leu Leu Thr Phe Gly Trp Ala His Thr Ser Met Asp Arg Asn Asn
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cgt ctt gaa cca gat aaa att act caa ata gat gca gtt aaa ggt tgg 1584
Arg Leu Glu Pro Asp Lys Ile Thr Gln Ile Asp Ala Val Lys Gly Trp
      515                      520                      525

ggg ggg aat atc ggg ttt gtc atc cca gga cct act ggg ggg aat ttg 1632
Gly Gly Asn Ile Gly Phe Val Ile Pro Gly Pro Thr Gly Gly Asn Leu
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gta aaa gtc agt gat agt tgg cat tca ctt aaa gtt caa gca cca caa 1680
Val Lys Val Ser Asp Ser Trp His Ser Leu Lys Val Gln Ala Pro Gln
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aga caa aca agt tat cgt att cgt ttg cgt tat gct tgt tta gtt acc 1728
Arg Gln Thr Ser Tyr Arg Ile Arg Leu Arg Tyr Ala Cys Leu Val Thr
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cat ggg gat gct att ttt gta gaa cac agc ggc agt agt cat ata gtt 1776
His Gly Asp Ala Ile Phe Val Glu His Ser Gly Ser Ser His Ile Val
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tca ttt ttt gat tgc tca aat tca tca ggt cgt cca tca aac act ctt 1824
Ser Phe Phe Asp Cys Ser Asn Ser Ser Gly Arg Pro Ser Asn Thr Leu
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cta gag agt gat ttt cgc tat att gat gtt cca ggt att ttt aca cca 1872
Leu Glu Ser Asp Phe Arg Tyr Ile Asp Val Pro Gly Ile Phe Thr Pro
      610                      615                      620

tca ata aat ccc tta ata aga tat aga aca caa agc ttt ggt acc cac 1920
Ser Ile Asn Pro Leu Ile Arg Tyr Arg Thr Gln Ser Phe Gly Thr His
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gcg ata gac aaa ttt gaa ttt att cca ctt aac act ttt ccg aat caa 1968
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      645                      650                      655

tca tta gaa aaa aga gaa cag gaa gta aat gat cta ttt atc aat taa 2016
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<211> 671

<212> PRT

<213> *Bacillus thuringiensis*

<400> 22

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Tyr Lys Glu Trp Leu Asn Met Cys Asp Ser Asn Thr Gln Phe Ile Gly
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Ala Val Leu Thr Gly Ile Asn Ser Val Gly Thr Ile Leu Ser Asn Leu
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Gly Val Pro Leu Ala Ser Gln Ser Phe Gly Ile Ile Ser Arg Leu Ile
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Gly Ile Leu Trp Ala Gly Pro Asp Pro Phe Glu Ala Leu Met Val Leu
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Val Glu Glu Leu Ile Lys Lys Ser Ile Asp Gln Arg Val Arg Glu Asn
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Leu	Val	Glu	Asn	Gly	Asn	Asp	Gly	Ser	Glu	Ile	Thr	His	Asn	Phe	Gly
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Ser	Val	Phe	Ser	Ile	Glu	Ser	Leu	Ala	Arg	Ile	Tyr	Leu	Gly	Gly	Thr
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 gct tta agt gta cga gat gct gtt tta acg ggt att aac agt gta ggg 192
 Ala Leu Ser Val Arg Asp Ala Val Leu Thr Gly Ile Asn Ser Val Gly
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 Thr Ile Leu Ser Asn Leu Gly Val Pro Leu Ala Ser Gln Ser Phe Gly
 65 70 75 80
 ata att agt agg cta ata ggt att tta tgg gca ggg cct gat cca ttt 288
 Ile Ile Ser Arg Leu Ile Gly Ile Leu Trp Ala Gly Pro Asp Pro Phe
 85 90 95
 gaa gca ctt atg gtt ctt gtt gaa gag ctt att aag aaa agt ata gat 336
 Glu Ala Leu Met Val Leu Val Glu Glu Leu Ile Lys Lys Ser Ile Asp
 100 105 110
 cag cgt gta aga gaa aat gct ctt aga gag cta gaa ggt tta cag gga 384
 Gln Arg Val Arg Glu Asn Ala Leu Arg Glu Leu Glu Gly Leu Gln Gly
 115 120 125
 att atg aga cta tat caa act aga ctg caa gca tgg cta gtt aac aag 432
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 Asn Phe Phe Glu Lys Asn Met Pro Lys Phe Lys Glu Arg Asn Phe Glu
 165 170 175
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 Ile Leu Leu Leu Pro Val Tyr Ala Gln Ala Ala Asn Leu His Leu Ile
 180 185 190
 tta tta aga gat gct gat tat ttt gga gca cag tgg caa tta ggt gat 624
 Leu Leu Arg Asp Ala Asp Tyr Phe Gly Ala Gln Trp Gln Leu Gly Asp
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gat atg aca tta aca gta tta gat ctc gca ata tta ttt cca aac tat	816
Asp Met Thr Leu Thr Val Leu Asp Leu Ala Ile Leu Phe Pro Asn Tyr	
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Asp Pro Arg Arg Tyr Pro Leu Ala Val Lys Thr Glu Leu Thr Arg Glu	
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Val Tyr Thr Asp Pro Val Gly Phe Thr Gly Val Leu Glu Ser Gly Gly	
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Phe Asn Phe Ala Asn Leu Ser Val Phe Ser Ile Glu Ser Leu Ala Arg	
385 390 395 400	
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Ile Tyr Leu Gly Gly Thr Glu Ala Asn Tyr Ile Thr Ser Gln Tyr	
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420 425 430	
gga tct tta aga tac gaa gtg cct gct aat ctt cca tcc caa act ata	1344
Gly Ser Leu Arg Tyr Glu Val Pro Ala Asn Leu Pro Ser Gln Thr Ile	
435 440 445	
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Leu Ser Glu Leu Pro Gly Lys Asp Lys Pro Arg Pro Asn Ala Gly Asp	
450 455 460	
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Phe Ser His Arg Leu Ser Tyr Ile Ser Asn Phe Asp Ala Arg Arg Ser	
465 470 475 480	
agt tca ggc ggt att gtt agt ctt tta acg ttt ggt tgg gca cat acc	1488
Ser Ser Gly Gly Ile Val Ser Leu Leu Thr Phe Gly Trp Ala His Thr	
485 490 495	

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Asp Ala Val Lys Gly Trp Gly Gly Asn Ile Gly Phe Val Ile Pro Gly
      515      520      525

cct act ggg ggg aat ttg gta aaa gtc agt gat agt tgg cat tca ctt 1632
Pro Thr Gly Gly Asn Leu Val Lys Val Ser Asp Ser Trp His Ser Leu
      530      535      540

aaa gtt caa gca cca caa aga caa aca agt tat cgt att cgt ttg cgt 1680
Lys Val Gln Ala Pro Gln Arg Gln Thr Ser Tyr Arg Ile Arg Leu Arg
545      550      555      560

tat gct tgt tta gtt acc cat ggg gat gct att ttt gta gaa cac agc 1728
Tyr Ala Cys Leu Val Thr His Gly Asp Ala Ile Phe Val Glu His Ser
      565      570      575

ggc agt agt cat ata gtt tca ttt ttt gat tgc tca aat tca tca ggt 1776
Gly Ser Ser His Ile Val Ser Phe Phe Asp Cys Ser Asn Ser Ser Gly
      580      585      590

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Arg Pro Ser Asn Thr Leu Leu Glu Ser Asp Phe Arg Tyr Ile Asp Val
      595      600      605

cca ggt att ttt aca cca tca ata aat ccc tta ata aga tat aga aca 1872
Pro Gly Ile Phe Thr Pro Ser Ile Asn Pro Leu Ile Arg Tyr Arg Thr
610      615      620

caa agc ttt ggt acc cac gcg ata gac aaa ttt gaa ttt att cca ctt 1920
Gln Ser Phe Gly Thr His Ala Ile Asp Lys Phe Glu Phe Ile Pro Leu
625      630      635      640

aac act ttt ccg aat caa tca tta gaa aaa aga gaa cag gaa gta aat 1968
Asn Thr Phe Pro Asn Gln Ser Leu Glu Lys Arg Glu Gln Glu Val Asn
      645      650      655

gat cta ttt atc aat taa 1986
Asp Leu Phe Ile Asn *
      660

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<210> 24
<211> 661
<212> PRT
<213> Bacillus thuringiensis

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<400> 24
Met Ser Asn Cys Tyr Pro Arg Tyr Pro Leu Ala Lys Asp Pro Gln Met
 1      5      10      15
Thr Met Arg Asn Thr Asn Tyr Lys Glu Trp Leu Asn Met Cys Asp Ser
20      25      30
Asn Thr Gln Phe Ile Gly Asp Ile Ser Thr Tyr Ser Ser Pro Glu Ala
35      40      45
Ala Leu Ser Val Arg Asp Ala Val Leu Thr Gly Ile Asn Ser Val Gly
50      55      60
Thr Ile Leu Ser Asn Leu Gly Val Pro Leu Ala Ser Gln Ser Phe Gly
65      70      75      80
Ile Ile Ser Arg Leu Ile Gly Ile Leu Trp Ala Gly Pro Asp Pro Phe
85      90      95
Glu Ala Leu Met Val Leu Val Glu Glu Leu Ile Lys Lys Ser Ile Asp
100      105      110
Gln Arg Val Arg Glu Asn Ala Leu Arg Glu Leu Glu Gly Leu Gln Gly
115      120      125
Ile Met Arg Leu Tyr Gln Thr Arg Leu Gln Ala Trp Leu Val Asn Lys

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130 135 140
 Asn Asp Asp Asn Arg Arg Ala Leu Val Thr Gln Tyr Ala Ile Val Asp
 145 150 155 160
 Asn Phe Phe Glu Lys Asn Met Pro Lys Phe Lys Glu Arg Asn Phe Glu
 165 170 175
 Ile Leu Leu Leu Pro Val Tyr Ala Gln Ala Ala Asn Leu His Leu Ile
 180 185 190
 Leu Leu Arg Asp Ala Asp Tyr Phe Gly Ala Gln Trp Gln Leu Gly Asp
 195 200 205
 Asp Glu Ile Arg Asp Asn Tyr Ile Arg Leu Gln Gly Leu Ile Arg Glu
 210 215 220
 Tyr Lys Asp His Cys Ile Thr Phe Tyr Asn Gln Gly Leu Asn Gln Phe
 225 230 235 240
 Asn Arg Ser Asn Ala Gln Asp Trp Val Ser Phe Asn Arg Phe Arg Thr
 245 250 255
 Asp Met Thr Leu Thr Val Leu Asp Leu Ala Ile Leu Phe Pro Asn Tyr
 260 265 270
 Asp Pro Arg Arg Tyr Pro Leu Ala Val Lys Thr Glu Leu Thr Arg Glu
 275 280 285
 Val Tyr Thr Asp Pro Val Gly Phe Thr Gly Val Leu Glu Ser Gly Gly
 290 295 300
 Arg Thr Tyr Pro Trp Tyr Asn Pro Asn Asn Thr Thr Phe Thr Ala Met
 305 310 315 320
 Glu Asn Asn Ala Arg Arg Arg Pro Ser Tyr Thr Thr Trp Leu Asn Arg
 325 330 335
 Ile Phe Val Tyr Thr Arg Thr Leu Gly Asn Met Ser Asp Val Arg Asn
 340 345 350
 Ile Trp Gly Gly His Thr Leu Val Glu Asn Gly Asn Asp Gly Ser Glu
 355 360 365
 Ile Thr His Asn Phe Gly Lys Thr Asp Ser Ile Thr Pro Ile Gln Tyr
 370 375 380
 Phe Asn Phe Ala Asn Leu Ser Val Phe Ser Ile Glu Ser Leu Ala Arg
 385 390 395 400
 Ile Tyr Leu Gly Gly Thr Glu Ala Asn Asn Tyr Ile Thr Ser Gln Tyr
 405 410 415
 Gly Val Ser Arg Val Ile Phe Asn Thr Ser Asn Ile Asn Asn Val Pro
 420 425 430
 Gly Ser Leu Arg Tyr Glu Val Pro Ala Asn Leu Pro Ser Gln Thr Ile
 435 440 445
 Leu Ser Glu Leu Pro Gly Lys Asp Lys Pro Arg Pro Asn Ala Gly Asp
 450 455 460
 Phe Ser His Arg Leu Ser Tyr Ile Ser Asn Phe Asp Ala Arg Arg Ser
 465 470 475 480
 Ser Ser Gly Gly Ile Val Ser Leu Leu Thr Phe Gly Trp Ala His Thr
 485 490 495
 Ser Met Asp Arg Asn Asn Arg Leu Glu Pro Asp Lys Ile Thr Gln Ile
 500 505 510
 Asp Ala Val Lys Gly Trp Gly Gly Asn Ile Gly Phe Val Ile Pro Gly
 515 520 525
 Pro Thr Gly Gly Asn Leu Val Lys Val Ser Asp Ser Trp His Ser Leu
 530 535 540
 Lys Val Gln Ala Pro Gln Arg Gln Thr Ser Tyr Arg Ile Arg Leu Arg
 545 550 555 560
 Tyr Ala Cys Leu Val Thr His Gly Asp Ala Ile Phe Val Glu His Ser
 565 570 575
 Gly Ser Ser His Ile Val Ser Phe Phe Asp Cys Ser Asn Ser Ser Gly
 580 585 590
 Arg Pro Ser Asn Thr Leu Leu Glu Ser Asp Phe Arg Tyr Ile Asp Val
 595 600 605
 Pro Gly Ile Phe Thr Pro Ser Ile Asn Pro Leu Ile Arg Tyr Arg Thr
 610 615 620
 Gln Ser Phe Gly Thr His Ala Ile Asp Lys Phe Glu Phe Ile Pro Leu
 625 630 635 640
 Asn Thr Phe Pro Asn Gln Ser Leu Glu Lys Arg Glu Gln Glu Val Asn
 645 650 655
 Asp Leu Phe Ile Asn
 660

<210> 25
 <211> 2145
 <212> DNA
 <213> *Bacillus thuringiensis*

<400> 25
 tttcaccaaa tataatgttt tttttagtaa acattgttac aggaatacat tggggtacta 60
 cgaatatata gaaagacacc tggcatatat ttattaggtg tcttaaaaat aaggactata 120
 taaggagtga aaaatatgaa ttcttatcaa aatacaaatg aatatgaaat tctggatggt 180
 tccccgaata acacaaatat gtcaaacaga tatccttttg caaaggatcc aaatatat 240
 cctattaacc tggacgcttg tcagggaagg ccatggcaag atacgtggga atcagtcctg 300
 gatatagtaa ctattgggac atacctata caattcttgc tagaaccggg tataggtgga 360
 attcctgtaa tttttcaat aataa caaa ctcattccgt cttctgggtca atctgtggca 420
 gcactttcta tatgtgattt agtatctata attcgtaaag aggtagacga gagcgtgtta 480
 agtgacgggg ttgcagattt tgagggtgaa atgactgctt atcaagatta ttatcttcat 540
 tatcttgagg attggcttac agataaatca aatcctaaaa aacttgctga cgtagttaaa 600
 cagttccaag cacgggaaga agatttctact aaacttttag cagggtcatt atcaagacag 660
 aaagctgaaa tattattatt gcctacgtat gtgcaagctg caaatgtgca tttattacta 720
 ttaagggacg cagttaaata taaaaaagaa tggggactag tgtgtccacc gttgtatcca 780
 ggggtcagga gaactgattg taacgagcgg ttaaaagcga aaataaaaga gtataactaa 840
 tattgtgtag ggtggtataa caagggttta gatcagataa gacaggcggg tacaagtgtc 900
 gaagtttggg cgaaatttaa taaatttcgt agagaaatga cgttggcggg attggatatt 960
 attgctatat ttccaactta tgattttgaa aaatatccat tagcaacaag tgtagagtta 1020
 actagggaaa tttatacaga tccagtgga tttcagggg gaaattatgg ttgggaacgg 1080
 ttttttagct ttaattcggg agaagcaaat ggaacacggg gacctgggtt agttacttgg 1140
 cttcaagcta tagatatata tagtcattct attaatcttc agcttggtta tcttagtggc 1200
 tgggggggaa ctgcgtatta tgaagacttc acaaagggtta acggtgcttt tcaacgtatg 1260
 tctggaacta cgagtaataa tccacgtaat attatttttg gcaataccga tatattttaa 1320
 attatttcat tagctagata tgcaatgcaa ccgtttgttg ggtattcaat cccacggcat 1380
 cttgtttcac gtgcagaatt ttttccgaca acactaaata ctttccgtga tgaggtaaac 1440
 agttctgggt actcacagac aattgaatct gtgttaccag gtattaataa ggatctacca 1500
 cctagtcgta caaattactc tcatagatta tcaaatgctg catgtgttca aaatgaaacc 1560
 tccagagtta acgtatttgg ttggacacat acaagtatga aaaaagataa tcgaatttat 1620
 ccagataaaa ttacgcaaat tctgcagta aaagcttttg ccctaccagc aggtacagga 1680
 tatgcaggag gttacgtcac agctgggcct ggttatacag gaggagatgt agtaacgtta 1740
 ccttatcaag caagtttaaa aatacgttta acttctgcac ccacgaataa aaattaccgt 1800
 gtttagacttc gctacgcgag tggaggacct ggtccgttcc gactagaaag atggtcgcca 1860
 agttctgttt caaatgctaa tttttctcgt ccagctacag gtggctatag ttcatttcat 1920
 tatgtggaca ccttagttac tacatttaac caatcaggtg ttgaaataat tatacaaaat 1980
 ctatctgggt accaccttat tgttgacaaa gtcgaattta tcccaattga catccaaatt 2040
 gaaaaatgta cgaaatgtca attcgaagga gacatatgta gatgtgaagg agtacaatcc 2100
 ttggaaacaa aaaaagagat tgtaaatagt ttatttatca attaa 2145

<210> 26
 <211> 2019
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> CDS
 <222> (1)...(2019)

<400> 26
 gtg aaa aat atg aat tct tat caa aat aca aat gaa tat gaa att ctg 48
 Met Lys Asn Met Asn Ser Tyr Gln Asn Thr Asn Glu Tyr Glu Ile Leu
 1 5 10 15
 gat ggt tcc ccg aat aac aca aat atg tca aac aga tat cct ttt gca 96
 Asp Gly Ser Pro Asn Asn Thr Asn Met Ser Asn Arg Tyr Pro Phe Ala
 20 25 30
 aag gat cca aat ata ttt cct att aac ctg gac gct tgt cag gga agg 144
 Lys Asp Pro Asn Ile Phe Pro Ile Asn Leu Asp Ala Cys Gln Gly Arg
 35 40 45
 cca tgg caa gat acg tgg gaa tca gtc tcg gat ata gta act att ggg 192
 Pro Trp Gln Asp Thr Trp Glu Ser Val Ser Asp Ile Val Thr Ile Gly

50	55	60	
aca tac ctt ata caa ttc ttg cta gaa ccc ggt ata ggt gga att cct			240
Thr Tyr Leu Ile Gln Phe Leu Leu Glu Pro Gly Ile Gly Gly Ile Pro			
65	70	75	80
gta ata ttt tca ata ata aac aaa ctc att ccg tct tct ggt caa tct			288
Val Ile Phe Ser Ile Ile Asn Lys Leu Ile Pro Ser Ser Gly Gln Ser			
	85	90	95
gtg gca gca ctt tct ata tgt gat tta gta tct ata att cgt aaa gag			336
Val Ala Ala Leu Ser Ile Cys Asp Leu Val Ser Ile Ile Arg Lys Glu			
	100	105	110
gta gac gag agc gtg tta agt gac ggg gtt gca gat ttt gag ggt gaa			384
Val Asp Glu Ser Val Leu Ser Asp Gly Val Ala Asp Phe Glu Gly Glu			
	115	120	125
atg act gct tat caa gat tat tat ctt cat tat ctt gag gat tgg ctt			432
Met Thr Ala Tyr Gln Asp Tyr Tyr Leu His Tyr Leu Glu Asp Trp Leu			
	130	135	140
aca gat aaa tca aat cct aaa aaa ctt gct gac gta gtt aaa cag ttc			480
Thr Asp Lys Ser Asn Pro Lys Lys Leu Ala Asp Val Val Lys Gln Phe			
	145	150	155
caa gca cgg gaa gaa gat ttc act aaa ctt tta gca ggg tca tta tca			528
Gln Ala Arg Glu Glu Asp Phe Thr Lys Leu Leu Ala Gly Ser Leu Ser			
	165	170	175
aga cag aaa gct gaa ata tta tta ttg cct acg tat gtg caa gct gca			576
Arg Gln Lys Ala Glu Ile Leu Leu Leu Pro Thr Tyr Val Gln Ala Ala			
	180	185	190
aat gtg cat tta tta cta tta agg gac gca gtt aaa tat aaa aaa gaa			624
Asn Val His Leu Leu Leu Leu Arg Asp Ala Val Lys Tyr Lys Lys Glu			
	195	200	205
tgg gga cta gtg tgt cca ccg ttg tat cca ggg tca ggg aga act gat			672
Trp Gly Leu Val Cys Pro Pro Leu Tyr Pro Gly Ser Gly Arg Thr Asp			
	210	215	220
tgt aac gag cgg tta aaa gcg aaa ata aaa gag tat act aat tat tgt			720
Cys Asn Glu Arg Leu Lys Ala Lys Ile Lys Glu Tyr Thr Asn Tyr Cys			
	225	230	235
gta ggg tgg tat aac aag ggt tta gat cag ata aga cag gcg ggt aca			768
Val Gly Trp Tyr Asn Lys Gly Leu Asp Gln Ile Arg Gln Ala Gly Thr			
	245	250	255
agt gct gaa gtt tgg tcg aaa ttt aat aaa ttt cgt aga gaa atg acg			816
Ser Ala Glu Val Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr			
	260	265	270
ttg gcg gta ttg gat att att gct ata ttt cca act tat gat ttt gaa			864
Leu Ala Val Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu			
	275	280	285
aaa tat cca tta gca aca agt gta gag tta act agg gaa att tat aca			912
Lys Tyr Pro Leu Ala Thr Ser Val Glu Leu Thr Arg Glu Ile Tyr Thr			
	290	295	300
gat cca gtg gga tat tca ggg gga aat tat ggt tgg gaa cgg ttt ttt			960
Asp Pro Val Gly Tyr Ser Gly Gly Asn Tyr Gly Trp Glu Arg Phe Phe			
	305	310	315
agc ttt aat tcg gta gaa gca aat gga aca cgg gga cct ggt tta gtt			1008
Ser Phe Asn Ser Val Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val			

325	330	335	
act tgg ctt caa gct ata gat ata tat agt cat tct att aat ctt cag Thr Trp Leu Gln Ala Ile Asp Ile Tyr Ser His Ser Ile Asn Leu Gln 340 345 350			1056
ctt ggt tat ctt agt ggc tgg ggg gga act cgt cat tat gaa gac ttc Leu Gly Tyr Leu Ser Gly Trp Gly Gly Thr Arg His Tyr Glu Asp Phe 355 360 365			1104
aca aag ggt aac ggt gct ttt caa cgt atg tct gga act acg agt aat Thr Lys Gly Asn Gly Ala Phe Gln Arg Met Ser Gly Thr Thr Ser Asn 370 375 380			1152
aat cca cgt aat att att ttt ggc aat acc gat ata ttt aaa att att Asn Pro Arg Asn Ile Ile Phe Gly Asn Thr Asp Ile Phe Lys Ile Ile 385 390 395 400			1200
tca tta gct aga tat gca atg caa ccg ttt gtt ggg tat tca atc cca Ser Leu Ala Arg Tyr Ala Met Gln Pro Phe Val Gly Tyr Ser Ile Pro 405 410 415			1248
cgg cat ctt gtt tca cgt gca gaa ttt ttt ccg aca aca cta aat act Arg His Leu Val Ser Arg Ala Glu Phe Phe Pro Thr Thr Leu Asn Thr 420 425 430			1296
ttc ctg tat gag gta aac agt tct ggg tac tca cag aca att gaa tct Phe Leu Tyr Glu Val Asn Ser Ser Gly Tyr Ser Gln Thr Ile Glu Ser 435 440 445			1344
gtg tta cca ggt att aat aag gat cta cca cct agt cgt aca aat tac Val Leu Pro Gly Ile Asn Lys Asp Leu Pro Pro Ser Arg Thr Asn Tyr 450 455 460			1392
tct cat aga tta tca aat gcg gca tgt gtt caa aat gaa acc tcc aga Ser His Arg Leu Ser Asn Ala Ala Cys Val Gln Asn Glu Thr Ser Arg 465 470 475 480			1440
gtt aac gta ttt ggt tgg aca cat aca agt atg aaa aaa gat aat cga Val Asn Val Phe Gly Trp Thr His Thr Ser Met Lys Lys Asp Asn Arg 485 490 495			1488
att tat cca gat aaa att acg caa att cct gca gta aaa gct ttt gcc Ile Tyr Pro Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Ala Phe Ala 500 505 510			1536
cta cca gca ggt aca gga tat gca gga ggt tac gtc aca gct ggg cct Leu Pro Ala Gly Thr Gly Tyr Ala Gly Gly Tyr Val Thr Ala Gly Pro 515 520 525			1584
ggt tat aca gga gga gat gta gta acg tta cct tat caa gca agt tta Gly Tyr Thr Gly Gly Asp Val Val Thr Leu Pro Tyr Gln Ala Ser Leu 530 535 540			1632
aaa ata cgt tta act tct gca ccc acg aat aaa aat tac cgt gtt aga Lys Ile Arg Leu Thr Ser Ala Pro Thr Asn Lys Asn Tyr Arg Val Arg 545 550 555 560			1680
ctt cgc tac gcg agt gga gga cct ggt ccg ttc cga gta gaa aga tgg Leu Arg Tyr Ala Ser Gly Gly Pro Gly Pro Phe Arg Val Glu Arg Trp 565 570 575			1728
tcg cca agt tct gtt tca aat gct aat ttt tct cgt cca gct aca ggt Ser Pro Ser Ser Val Ser Asn Ala Asn Phe Ser Arg Pro Ala Thr Gly 580 585 590			1776
ggc tat agt tca ttt gat tat gtg gac acc tta gtt act aca ttt aat Gly Tyr Ser Ser Phe Asp Tyr Val Asp Thr Leu Val Thr Thr Phe Asn			1824

595	600	605	
caa tca ggt gtt gaa ata att ata caa aat cta tct ggt tac cac ctt			1872
Gln Ser Gly Val Glu Ile Ile Ile Gln Asn Leu Ser Gly Tyr His Leu			
610	615	620	
att gtt gac aaa gtc gaa ttt atc cca att gac atc caa att gaa aaa			1920
Ile Val Asp Lys Val Glu Phe Ile Pro Ile Asp Ile Gln Ile Glu Lys			
625	630	635	640
tgt acg aaa tgt caa ttc gaa gga gac ata tgt aga tgt gaa gga gta			1968
Cys Thr Lys Cys Gln Phe Glu Gly Asp Ile Cys Arg Cys Glu Gly Val			
645	650	655	
caa tcc ttg gaa aca aaa aaa gag att gta aat agt tta ttt atc aat			2016
Gln Ser Leu Glu Thr Lys Lys Glu Ile Val Asn Ser Leu Phe Ile Asn			
660	665	670	
taa			2019
*			

<210> 27
 <211> 672
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 27

Met Lys Asn Met Asn Ser Tyr Gln Asn Thr Asn Glu Tyr Glu Ile Leu			
1	5	10	15
Asp Gly Ser Pro Asn Asn Thr Asn Met Ser Asn Arg Tyr Pro Phe Ala			
20	25	30	
Lys Asp Pro Asn Ile Phe Pro Ile Asn Leu Asp Ala Cys Gln Gly Arg			
35	40	45	
Pro Trp Gln Asp Thr Trp Glu Ser Val Ser Asp Ile Val Thr Ile Gly			
50	55	60	
Thr Tyr Leu Ile Gln Phe Leu Leu Glu Pro Gly Ile Gly Gly Ile Pro			
65	70	75	80
Val Ile Phe Ser Ile Ile Asn Lys Leu Ile Pro Ser Ser Gly Gln Ser			
85	90	95	
Val Ala Ala Leu Ser Ile Cys Asp Leu Val Ser Ile Ile Arg Lys Glu			
100	105	110	
Val Asp Glu Ser Val Leu Ser Asp Gly Val Ala Asp Phe Glu Gly Glu			
115	120	125	
Met Thr Ala Tyr Gln Asp Tyr Tyr Leu His Tyr Leu Glu Asp Trp Leu			
130	135	140	
Thr Asp Lys Ser Asn Pro Lys Lys Leu Ala Asp Val Val Lys Gln Phe			
145	150	155	160
Gln Ala Arg Glu Glu Asp Phe Thr Lys Leu Leu Ala Gly Ser Leu Ser			
165	170	175	
Arg Gln Lys Ala Glu Ile Leu Leu Leu Pro Thr Tyr Val Gln Ala Ala			
180	185	190	
Asn Val His Leu Leu Leu Leu Arg Asp Ala Val Lys Tyr Lys Lys Glu			
195	200	205	
Trp Gly Leu Val Cys Pro Pro Leu Tyr Pro Gly Ser Gly Arg Thr Asp			
210	215	220	
Cys Asn Glu Arg Leu Lys Ala Lys Ile Lys Glu Tyr Thr Asn Tyr Cys			
225	230	235	240
Val Gly Trp Tyr Asn Lys Gly Leu Asp Gln Ile Arg Gln Ala Gly Thr			
245	250	255	
Ser Ala Glu Val Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr			
260	265	270	
Leu Ala Val Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu			
275	280	285	
Lys Tyr Pro Leu Ala Thr Ser Val Glu Leu Thr Arg Glu Ile Tyr Thr			
290	295	300	
Asp Pro Val Gly Tyr Ser Gly Gly Asn Tyr Gly Trp Glu Arg Phe Phe			

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305          310          315          320
Ser Phe Asn Ser Val Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val
          325          330          335
Thr Trp Leu Gln Ala Ile Asp Ile Tyr Ser His Ser Ile Asn Leu Gln
          340          345          350
Leu Gly Tyr Leu Ser Gly Trp Gly Gly Thr Arg His Tyr Glu Asp Phe
          355          360          365
Thr Lys Gly Asn Gly Ala Phe Gln Arg Met Ser Gly Thr Thr Ser Asn
          370          375          380
Asn Pro Arg Asn Ile Ile Phe Gly Asn Thr Asp Ile Phe Lys Ile Ile
385          390          395          400
Ser Leu Ala Arg Tyr Ala Met Gln Pro Phe Val Gly Tyr Ser Ile Pro
          405          410          415
Arg His Leu Val Ser Arg Ala Glu Phe Phe Pro Thr Thr Leu Asn Thr
          420          425          430
Phe Leu Tyr Glu Val Asn Ser Ser Gly Tyr Ser Gln Thr Ile Glu Ser
          435          440          445
Val Leu Pro Gly Ile Asn Lys Asp Leu Pro Pro Ser Arg Thr Asn Tyr
          450          455          460
Ser His Arg Leu Ser Asn Ala Ala Cys Val Gln Asn Glu Thr Ser Arg
465          470          475          480
Val Asn Val Phe Gly Trp Thr His Thr Ser Met Lys Lys Asp Asn Arg
          485          490          495
Ile Tyr Pro Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Ala Phe Ala
          500          505          510
Leu Pro Ala Gly Thr Gly Tyr Ala Gly Gly Tyr Val Thr Ala Gly Pro
          515          520          525
Gly Tyr Thr Gly Gly Asp Val Val Thr Leu Pro Tyr Gln Ala Ser Leu
          530          535          540
Lys Ile Arg Leu Thr Ser Ala Pro Thr Asn Lys Asn Tyr Arg Val Arg
545          550          555          560
Leu Arg Tyr Ala Ser Gly Gly Pro Gly Pro Phe Arg Val Glu Arg Trp
          565          570          575
Ser Pro Ser Ser Val Ser Asn Ala Asn Phe Ser Arg Pro Ala Thr Gly
          580          585          590
Gly Tyr Ser Ser Phe Asp Tyr Val Asp Thr Leu Val Thr Thr Phe Asn
          595          600          605
Gln Ser Gly Val Glu Ile Ile Ile Gln Asn Leu Ser Gly Tyr His Leu
          610          615          620
Ile Val Asp Lys Val Glu Phe Ile Pro Ile Asp Ile Gln Ile Glu Lys
625          630          635          640
Cys Thr Lys Cys Gln Phe Glu Gly Asp Ile Cys Arg Cys Glu Gly Val
          645          650          655
Gln Ser Leu Glu Thr Lys Lys Glu Ile Val Asn Ser Leu Phe Ile Asn
          660          665          670

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<210> 28
 <211> 2010
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> CDS
 <222> (1)...(2010)

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<400> 28
atg aat tct tat caa aat aca aat gaa tat gaa att ctg gat ggt tcc 48
Met Asn Ser Tyr Gln Asn Thr Asn Glu Tyr Glu Ile Leu Asp Gly Ser
  1          5          10          15

ccg aat aac aca aat atg tca aac aga tat cct ttt gca aag gat cca 96
Pro Asn Asn Thr Asn Met Ser Asn Arg Tyr Pro Phe Ala Lys Asp Pro
  20          25          30

aat ata ttt cct att aac ctg gac gct tgt cag gga agg cca tgg caa 144
Asn Ile Phe Pro Ile Asn Leu Asp Ala Cys Gln Gly Arg Pro Trp Gln
  35          40          45

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gat acg tgg gaa tca gtc tcg gat ata gta act att ggg aca tac ctt	192
Asp Thr Trp Glu Ser Val Ser Asp Ile Val Thr Ile Gly Thr Tyr Leu	
50 55 60	
ata caa ttc ttg cta gaa ccc ggt ata ggt gga att cct gta ata ttt	240
Ile Gln Phe Leu Leu Glu Pro Gly Ile Gly Gly Ile Pro Val Ile Phe	
65 70 75 80	
tca ata ata aac aaa ctc att ccg tct tct ggt caa tct gtg gca gca	288
Ser Ile Ile Asn Lys Leu Ile Pro Ser Ser Gly Gln Ser Val Ala Ala	
85 90 95	
ctt tct ata tgt gat tta gta tct ata att cgt aaa gag gta gac gag	336
Leu Ser Ile Cys Asp Leu Val Ser Ile Ile Arg Lys Glu Val Asp Glu	
100 105 110	
agc gtg tta agt gac ggg gtt gca gat ttt gag ggt gaa atg act gct	384
Ser Val Leu Ser Asp Gly Val Ala Asp Phe Glu Gly Glu Met Thr Ala	
115 120 125	
tat caa gat tat tat ctt cat tat ctt gag gat tgg ctt aca gat aaa	432
Tyr Gln Asp Tyr Tyr Leu His Tyr Leu Glu Asp Trp Leu Thr Asp Lys	
130 135 140	
tca aat cct aaa aaa ctt gct gac gta gtt aaa cag ttc caa gca cgg	480
Ser Asn Pro Lys Lys Leu Ala Asp Val Val Lys Gln Phe Gln Ala Arg	
145 150 155 160	
gaa gaa gat ttc act aaa ctt tta gca ggg tca tta tca aga cag aaa	528
Glu Glu Asp Phe Thr Lys Leu Leu Ala Gly Ser Leu Ser Arg Gln Lys	
165 170 175	
gct gaa ata tta tta ttg cct acg tat gtg caa gct gca aat gtg cat	576
Ala Glu Ile Leu Leu Leu Pro Thr Tyr Val Gln Ala Ala Asn Val His	
180 185 190	
tta tta cta tta agg gac gca gtt aaa tat aaa gaa tgg gga cta	624
Leu Leu Leu Leu Arg Asp Ala Val Lys Tyr Lys Lys Glu Trp Gly Leu	
195 200 205	
gtg tgt cca ccg ttg tat cca ggg tca ggg aga act gat tgt aac gag	672
Val Cys Pro Pro Leu Tyr Pro Gly Ser Gly Arg Thr Asp Cys Asn Glu	
210 215 220	
cgg tta aaa gcg aaa ata aaa gag tat act aat tat tgt gta ggg tgg	720
Arg Leu Lys Ala Lys Ile Lys Glu Tyr Thr Asn Tyr Cys Val Gly Trp	
225 230 235 240	
tat aac aag ggt tta gat cag ata aga cag gcg ggt aca agt gct gaa	768
Tyr Asn Lys Gly Leu Asp Gln Ile Arg Gln Ala Gly Thr Ser Ala Glu	
245 250 255	
gtt tgg tcg aaa ttt aat aaa ttt cgt aga gaa atg acg ttg gcg gta	816
Val Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Ala Val	
260 265 270	
ttg gat att att gct ata ttt cca act tat gat ttt gaa aaa tat cca	864
Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys Tyr Pro	
275 280 285	
tta gca aca agt gta gag tta act agg gaa att tat aca gat cca gtg	912
Leu Ala Thr Ser Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Pro Val	
290 295 300	
gga tat tca ggg gga aat tat ggt tgg gaa cgg ttt ttt agc ttt aat	960
Gly Tyr Ser Gly Gly Asn Tyr Gly Trp Glu Arg Phe Phe Ser Phe Asn	
305 310 315 320	

tcg gta gaa gca aat gga aca cgg gga cct ggt tta gtt act tgg ctt	1008
Ser Val Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp Leu	
325 330 335	
caa gct ata gat ata tat agt cat tct att aat ctt cag ctt ggt tat	1056
Gln Ala Ile Asp Ile Tyr Ser His Ser Ile Asn Leu Gln Leu Gly Tyr	
340 345 350	
ctt agt ggc tgg ggg gga act cgt cat tat gaa gac ttc aca aag ggt	1104
Leu Ser Gly Trp Gly Gly Thr Arg His Tyr Glu Asp Phe Thr Lys Gly	
355 360 365	
aac ggt gct ttt caa cgt atg tct gga act acg agt aat aat cca cgt	1152
Asn Gly Ala Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asn Pro Arg	
370 375 380	
aat att att ttt ggc aat acc gat ata ttt aaa att att tca tta gct	1200
Asn Ile Ile Phe Gly Asn Thr Asp Ile Phe Lys Ile Ile Ser Leu Ala	
385 390 395 400	
aga tat gca atg caa ccg ttt gtt ggg tat tca atc cca cgg cat ctt	1248
Arg Tyr Ala Met Gln Pro Phe Val Gly Tyr Ser Ile Pro Arg His Leu	
405 410 415	
gtt tca cgt gca gaa ttt ttt ccg aca aca cta aat act ttc ctg tat	1296
Val Ser Arg Ala Glu Phe Phe Pro Thr Thr Leu Asn Thr Phe Leu Tyr	
420 425 430	
gag gta aac agt tct ggg tac tca cag aca att gaa tct gtg tta cca	1344
Glu Val Asn Ser Ser Gly Tyr Ser Gln Thr Ile Glu Ser Val Leu Pro	
435 440 445	
ggg att aat aag gat cta cca cct agt cgt aca aat tac tct cat aga	1392
Gly Ile Asn Lys Asp Leu Pro Pro Ser Arg Thr Asn Tyr Ser His Arg	
450 455 460	
tta tca aat gcg gca tgt gtt caa aat gaa acc tcc aga gtt aac gta	1440
Leu Ser Asn Ala Ala Cys Val Gln Asn Glu Thr Ser Arg Val Asn Val	
465 470 475 480	
ttt ggt tgg aca cat aca agt atg aaa aaa gat aat cga att tat cca	1488
Phe Gly Trp Thr His Thr Ser Met Lys Lys Asp Asn Arg Ile Tyr Pro	
485 490 495	
gat aaa att acg caa att cct gca gta aaa gct ttt gcc cta cca gca	1536
Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Ala Phe Ala Leu Pro Ala	
500 505 510	
ggg aca gga tat gca gga ggt tac gtc aca gct ggg cct ggt tat aca	1584
Gly Thr Gly Tyr Ala Gly Gly Tyr Val Thr Ala Gly Pro Gly Tyr Thr	
515 520 525	
gga gga gat gta gta acg tta cct tat caa gca agt tta aaa ata cgt	1632
Gly Gly Asp Val Val Thr Leu Pro Tyr Gln Ala Ser Leu Lys Ile Arg	
530 535 540	
tta act tct gca ccc acg aat aaa aat tac cgt gtt aga ctt cgc tac	1680
Leu Thr Ser Ala Pro Thr Asn Lys Asn Tyr Arg Val Arg Leu Arg Tyr	
545 550 555 560	
gcg agt gga gga cct ggt ccg ttc cga gta gaa aga tgg tcg cca agt	1728
Ala Ser Gly Gly Pro Gly Pro Phe Arg Val Glu Arg Trp Ser Pro Ser	
565 570 575	
tct gtt tca aat gct aat ttt tct cgt cca gct aca ggt ggc tat agt	1776
Ser Val Ser Asn Ala Asn Phe Ser Arg Pro Ala Thr Gly Gly Tyr Ser	
580 585 590	

tca ttt gat tat gtg gac acc tta gtt act aca ttt aat caa tca ggt 1824
 Ser Phe Asp Tyr Val Asp Thr Leu Val Thr Thr Phe Asn Gln Ser Gly
 595 600 605

gtt gaa ata att ata caa aat cta tct ggt tac cac ctt att gtt gac 1872
 Val Glu Ile Ile Ile Gln Asn Leu Ser Gly Tyr His Leu Ile Val Asp
 610 615 620

aaa gtc gaa ttt atc cca att gac atc caa att gaa aaa tgt acg aaa 1920
 Lys Val Glu Phe Ile Pro Ile Asp Ile Gln Ile Glu Lys Cys Thr Lys
 625 630 635 640

tgt caa ttc gaa gga gac ata tgt aga tgt gaa gga gta caa tcc ttg 1968
 Cys Gln Phe Glu Gly Asp Ile Cys Arg Cys Glu Gly Val Gln Ser Leu
 645 650 655

gaa aca aaa aaa gag att gta aat agt tta ttt atc aat taa 2010
 Glu Thr Lys Lys Glu Ile Val Asn Ser Leu Phe Ile Asn *
 660 665

<210> 29

<211> 669

<212> PRT

<213> Bacillus thuringiensis

<400> 29

Met Asn Ser Tyr Gln Asn Thr Asn Glu Tyr Glu Ile Leu Asp Gly Ser
 1 5 10 15
 Pro Asn Asn Thr Asn Met Ser Asn Arg Tyr Pro Phe Ala Lys Asp Pro
 20 25 30
 Asn Ile Phe Pro Ile Asn Leu Asp Ala Cys Gln Gly Arg Pro Trp Gln
 35 40 45
 Asp Thr Trp Glu Ser Val Ser Asp Ile Val Thr Ile Gly Thr Tyr Leu
 50 55 60
 Ile Gln Phe Leu Leu Glu Pro Gly Ile Gly Gly Ile Pro Val Ile Phe
 65 70 75 80
 Ser Ile Ile Asn Lys Leu Ile Pro Ser Ser Gly Gln Ser Val Ala Ala
 85 90 95
 Leu Ser Ile Cys Asp Leu Val Ser Ile Ile Arg Lys Glu Val Asp Glu
 100 105 110
 Ser Val Leu Ser Asp Gly Val Ala Asp Phe Glu Gly Glu Met Thr Ala
 115 120 125
 Tyr Gln Asp Tyr Tyr Leu His Tyr Leu Glu Asp Trp Leu Thr Asp Lys
 130 135 140
 Ser Asn Pro Lys Lys Leu Ala Asp Val Val Lys Gln Phe Gln Ala Arg
 145 150 155 160
 Glu Glu Asp Phe Thr Lys Leu Leu Ala Gly Ser Leu Ser Arg Gln Lys
 165 170 175
 Ala Glu Ile Leu Leu Leu Pro Thr Tyr Val Gln Ala Ala Asn Val His
 180 185 190
 Leu Leu Leu Leu Arg Asp Ala Val Lys Tyr Lys Lys Glu Trp Gly Leu
 195 200 205
 Val Cys Pro Pro Leu Tyr Pro Gly Ser Gly Arg Thr Asp Cys Asn Glu
 210 215 220
 Arg Leu Lys Ala Lys Ile Lys Glu Tyr Thr Asn Tyr Cys Val Gly Trp
 225 230 235 240
 Tyr Asn Lys Gly Leu Asp Gln Ile Arg Gln Ala Gly Thr Ser Ala Glu
 245 250 255
 Val Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Ala Val
 260 265 270
 Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys Tyr Pro
 275 280 285
 Leu Ala Thr Ser Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Pro Val
 290 295 300
 Gly Tyr Ser Gly Gly Asn Tyr Gly Trp Glu Arg Phe Phe Ser Phe Asn


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305          310          315          320
Ser Val Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp Leu
          325          330          335
Gln Ala Ile Asp Ile Tyr Ser His Ser Ile Asn Leu Gln Leu Gly Tyr
          340          345          350
Leu Ser Gly Trp Gly Gly Thr Arg His Tyr Glu Asp Phe Thr Lys Gly
          355          360          365
Asn Gly Ala Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asn Pro Arg
          370          375          380
Asn Ile Ile Phe Gly Asn Thr Asp Ile Phe Lys Ile Ile Ser Leu Ala
385          390          395          400
Arg Tyr Ala Met Gln Pro Phe Val Gly Tyr Ser Ile Pro Arg His Leu
          405          410          415
Val Ser Arg Ala Glu Phe Phe Pro Thr Thr Leu Asn Thr Phe Leu Tyr
          420          425          430
Glu Val Asn Ser Ser Gly Tyr Ser Gln Thr Ile Glu Ser Val Leu Pro
          435          440          445
Gly Ile Asn Lys Asp Leu Pro Pro Ser Arg Thr Asn Tyr Ser His Arg
          450          455          460
Leu Ser Asn Ala Ala Cys Val Gln Asn Glu Thr Ser Arg Val Asn Val
465          470          475          480
Phe Gly Trp Thr His Thr Ser Met Lys Lys Asp Asn Arg Ile Tyr Pro
          485          490          495
Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Ala Phe Ala Leu Pro Ala
          500          505          510
Gly Thr Gly Tyr Ala Gly Gly Tyr Val Thr Ala Gly Pro Gly Tyr Thr
          515          520          525
Gly Gly Asp Val Val Thr Leu Pro Tyr Gln Ala Ser Leu Lys Ile Arg
          530          535          540
Leu Thr Ser Ala Pro Thr Asn Lys Asn Tyr Arg Val Arg Leu Arg Tyr
545          550          555          560
Ala Ser Gly Gly Pro Gly Pro Phe Arg Val Glu Arg Trp Ser Pro Ser
          565          570          575
Ser Val Ser Asn Ala Asn Phe Ser Arg Pro Ala Thr Gly Gly Tyr Ser
          580          585          590
Ser Phe Asp Tyr Val Asp Thr Leu Val Thr Thr Phe Asn Gln Ser Gly
          595          600          605
Val Glu Ile Ile Ile Gln Asn Leu Ser Gly Tyr His Leu Ile Val Asp
          610          615          620
Lys Val Glu Phe Ile Pro Ile Asp Ile Gln Ile Glu Lys Cys Thr Lys
625          630          635          640
Cys Gln Phe Glu Gly Asp Ile Cys Arg Cys Glu Gly Val Gln Ser Leu
          645          650          655
Glu Thr Lys Lys Glu Ile Val Asn Ser Leu Phe Ile Asn
          660          665

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<210> 30

<211> 1176

<212> PRT

<213> Bacillus thuringiensis

<400> 30

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Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
1          5          10          15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
          20          25          30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
          35          40          45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
          50          55          60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Pro Val Gln Ile
65          70          75          80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
          85          90          95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
          100          105          110
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu

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Ala Lys Arg	660	Arg Asn Leu	665	Leu Leu Gln	670	Asp Pro Asn Phe
675		680		685		
Arg Gly Ile	Asn Arg Gln	Leu Asp Arg	Gly Trp Arg	Gly Ser Thr	Asp	
690		695		700		
Ile Thr Ile	Gln Gly Gly	Asp Asp Val	Phe Lys Glu	Asn Tyr Val	Thr	
705		710		715		720
Leu Leu Gly	Thr Phe Asp	Glu Cys Tyr	Pro Thr Tyr	Leu Tyr Gln	Lys	
	725		730		735	
Ile Asp Glu	Ser Lys Leu	Lys Ala Tyr	Thr Arg Tyr	Gln Leu Arg	Gly	
	740		745		750	
Tyr Ile Glu	Asp Ser Gln	Asp Leu Glu	Ile Tyr Leu	Ile Arg Tyr	Asn	
	755		760		765	
Ala Lys His	Glu Thr Val	Asn Val Pro	Gly Thr Gly	Ser Leu Trp	Pro	
770		775		780		
Leu Ser Ala	Gln Ser Pro	Ile Gly Lys	Cys Gly Glu	Pro Asn Arg	Cys	
785		790		795		800
Ala Pro His	Leu Glu Trp	Asn Pro Asp	Leu Asp Cys	Ser Cys Arg	Asp	
	805		810		815	
Gly Glu Lys	Cys Ala His	His Ser His	Phe Ser Leu	Asp Ile Asp		
	820		825		830	
Val Gly Cys	Thr Asp Leu	Asn Glu Asp	Leu Gly Val	Trp Val Ile	Phe	
	835		840		845	
Lys Ile Lys	Thr Gln Asp	Gly His Ala	Arg Leu Gly	Asn Leu Glu	Phe	
	850		855		860	
Leu Glu Glu	Lys Pro Leu	Val Gly Glu	Ala Leu Ala	Arg Val Lys	Arg	
865		870		875		880
Ala Glu Lys	Lys Trp Arg	Asp Lys Arg	Glu Lys Leu	Glu Trp Glu	Thr	
	885		890		895	
Asn Ile Val	Tyr Lys Glu	Ala Lys Glu	Ser Val Asp	Ala Leu Phe	Val	
	900		905		910	
Asn Ser Gln	Tyr Asp Gln	Leu Gln Ala	Asp Thr Asn	Ile Ala Met	Ile	
	915		920		925	
His Ala Ala	Asp Lys Arg	Val His Ser	Ile Arg Glu	Ala Tyr Leu	Pro	
930		935		940		
Glu Leu Ser	Val Ile Pro	Gly Val Asn	Ala Ala Ile	Phe Glu Glu	Leu	
945		950		955		960
Glu Gly Arg	Ile Phe Thr	Ala Phe Ser	Leu Tyr Asp	Ala Arg Asn	Val	
	965		970		975	
Ile Lys Asn	Gly Asp Phe	Asn Asn Gly	Leu Ser Cys	Trp Asn Val	Lys	
	980		985		990	
Gly His Val	Asp Val Glu	Glu Gln Asn	Asn Gln Arg	Ser Val Leu	Val	
	995		1000		1005	
Val Pro Glu	Trp Glu Ala	Glu Val Ser	Gln Glu Val	Arg Val Cys	Pro	
	1010		1015		1020	
Gly Arg Gly	Tyr Ile Leu	Arg Val Thr	Ala Tyr Lys	Glu Gly Tyr	Gly	
1025		1030		1035		1040
Glu Gly Cys	Val Thr Ile	His Glu Ile	Glu Asn Asn	Thr Asp Glu	Leu	
	1045		1050		1055	
Lys Phe Ser	Asn Cys Val	Glu Glu Glu	Ile Tyr Pro	Asn Asn Thr	Val	
	1060		1065		1070	
Thr Cys Asn	Asp Tyr Thr	Val Asn Gln	Glu Glu Tyr	Gly Gly Ala	Tyr	
	1075		1080		1085	
Thr Ser Arg	Asn Arg Gly	Tyr Asn Glu	Ala Pro Ser	Val Pro Ala	Asp	
	1090		1095		1100	
Tyr Ala Ser	Val Tyr Glu	Lys Ser Tyr	Thr Asp Gly	Arg Arg Glu		
1105		1110		1115		1120
Asn Pro Cys	Glu Phe Asn	Arg Gly Tyr	Arg Asp Tyr	Thr Pro Leu	Pro	
	1125		1130		1135	
Val Gly Tyr	Val Thr Lys	Glu Leu Glu	Tyr Phe Pro	Glu Thr Asp	Lys	
	1140		1145		1150	
Val Trp Ile	Glu Ile Gly	Glu Thr Glu	Gly Thr Phe	Ile Val Asp	Ser	
	1155		1160		1165	
Val Glu Leu	Leu Leu Met	Glu Glu				
	1170		1175			

<210> 31

<211> 1178

<212> PRT

<213> *Bacillus thuringiensis*

<400> 31

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Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
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Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20          25          30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
 35          40          45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
 50          55          60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
 65          70          75          80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
 85          90          95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100          105          110
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
115          120          125
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130          135          140
Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145          150          155          160
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
165          170          175
Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180          185          190
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195          200          205
Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210          215          220
Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225          230          235          240
Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245          250          255
Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260          265          270
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275          280          285
Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290          295          300
Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
305          310          315          320
Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325          330          335
Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340          345          350
Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355          360          365
Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370          375          380
Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385          390          395          400
Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405          410          415
Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420          425          430
Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435          440          445
Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450          455          460
Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
465          470          475          480
Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
485          490          495
Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly

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1045 1050 1055
 Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr Pro Asn Asn
 1060 1065 1070
 Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu Glu Tyr Gly Gly
 1075 1080 1085
 Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro
 1090 1095 1100
 Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg
 1105 1110 1115 1120
 Arg Glu Asn Pro Cys Glu Phe Asn Arg Gly Tyr Arg Asp Tyr Thr Pro
 1125 1130 1135
 Leu Pro Val Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
 1140 1145 1150
 Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val
 1155 1160 1165
 Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1170 1175

<210> 32

<211> 1189

<212> PRT

<213> *Bacillus thuringiensis*

<400> 32

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
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 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30
 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45
 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60
 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80
 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95
 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
 100 105 110
 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
 115 120 125
 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
 130 135 140
 Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
 145 150 155 160
 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
 165 170 175
 Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
 180 185 190
 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
 195 200 205
 Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
 210 215 220
 Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
 225 230 235 240
 Asp Ile Ala Ala Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
 245 250 255
 Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
 260 265 270
 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
 275 280 285
 Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
 290 295 300
 Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
 305 310 315 320
 Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
 325 330 335
 Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg

340 345 350
 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365
 Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 370 375 380
 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400
 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415
 Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430
 Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
 435 440 445
 Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
 450 455 460
 Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
 465 470 475 480
 Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
 485 490 495
 Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
 500 505 510
 Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
 515 520 525
 Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
 530 535 540
 Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
 545 550 555 560
 Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
 565 570 575
 Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
 580 585 590
 Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
 595 600 605
 Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
 610 615 620
 Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
 625 630 635 640
 Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
 645 650 655
 Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
 660 665 670
 Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
 675 680 685
 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
 690 695 700
 Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
 705 710 715 720
 Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
 725 730 735
 Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
 740 745 750
 Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
 755 760 765
 Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
 770 775 780
 Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 785 790 795 800
 Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
 805 810 815
 Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
 820 825 830
 Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845
 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 850 855 860
 His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880
 Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp

885 890 895
 Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910
 Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
 915 920 925
 Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
 930 935 940
 His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 945 950 955 960
 Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
 965 970 975
 Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 980 985 990
 Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005
 Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020
 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040
 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055
 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070
 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085
 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100
 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120
 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135
 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150
 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180
 Leu Leu Met Glu Glu
 1185

<210> 33

<211> 719

<212> PRT

<213> *Bacillus thuringiensis*

<400> 33

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
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 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35 40 45
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95
 Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
 100 105 110
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
 115 120 125
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
 130 135 140
 Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe

- 64 -

705

710

715

<210> 34
 <211> 633
 <212> PRT
 <213> Bacillus thuringiensis

<400> 34

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Met Asn Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala Tyr
 1           5           10           15
Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp
      20           25           30
Thr Ile Gln Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
      35           40           45
Tyr Val Ala Pro Val Val Gly Thr Val Ser Ser Phe Leu Leu Lys Lys
      50           55           60
Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly Ile
      65           70           75           80
Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu
      85           90           95
Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
      100          105          110
Val Asn Ala Glu Leu Ile Gly Leu Gln Ala Asn Ile Arg Glu Phe Asn
      115          120          125
Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro Leu
      130          135          140
Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg
      145          150          155          160
Leu Pro Gln Phe Gln Ile Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu
      165          170          175
Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val Ile
      180          185          190
Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr
      195          200          205
Arg Asp Tyr Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile
      210          215          220
Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp
      225          230          235          240
Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val
      245          250          255
Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Met Val Ser Ser Gly
      260          265          270
Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe
      275          280          285
Thr Ala Gln Asn Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser
      290          295          300
Asn Tyr Ile Leu Ser Gly Ile Ser Gly Thr Arg Leu Ser Ile Thr Phe
      305          310          315          320
Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ser Leu Asn
      325          330          335
Ser Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Leu Ile Gly
      340          345          350
Ala Thr Asn Leu Asn His Asn Phe Asn Cys Ser Thr Val Leu Pro Pro
      355          360          365
Leu Ser Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Thr Asp Arg
      370          375          380
Glu Gly Val Ala Thr Ser Thr Asn Trp Gln Thr Glu Ser Phe Gln Thr
      385          390          395          400
Thr Leu Ser Leu Arg Cys Gly Ala Phe Ser Ala Arg Gly Asn Ser Asn
      405          410          415
Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val
      420          425          430
Ile Arg Asn Glu Asp Leu Thr Arg Pro Leu His Tyr Asn Gln Ile Arg
      435          440          445
Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr Leu
      450          455          460
Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Ala Asn Glu Asn

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465 470 475 480
 Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile
 485 490 495
 Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile
 500 505 510
 Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser
 515 520 525
 Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn
 530 535 540
 Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr
 545 550 555 560
 Ile Asn Gly Arg Val Tyr Thr Val Ser Asn Val Asn Thr Thr Thr Asn
 565 570 575
 Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile
 580 585 590
 Gly Asn Ile Val Ala Ser Asp Asn Thr Asn Val Thr Leu Asp Ile Asn
 595 600 605
 Val Thr Leu Asn Ser Gly Thr Pro Phe Asp Leu Met Asn Ile Met Phe
 610 615 620
 Val Pro Thr Asn Leu Pro Pro Leu Tyr
 625 630

<210> 35
 <211> 652
 <212> PRT
 <213> Bacillus thuringiensis

<400> 35
 Met Ile Arg Lys Gly Gly Arg Lys Met Asn Pro Asn Asn Arg Ser Glu
 1 5 10 15
 His Asp Thr Ile Lys Thr Thr Glu Asn Asn Glu Val Pro Thr Asn His
 20 25 30
 Val Gln Tyr Pro Leu Ala Glu Thr Pro Asn Pro Thr Leu Glu Asp Leu
 35 40 45
 Asn Tyr Lys Glu Phe Leu Arg Met Thr Ala Asp Asn Asn Thr Glu Ala
 50 55 60
 Leu Asp Ser Ser Thr Thr Lys Asp Val Ile Gln Lys Gly Ile Ser Val
 65 70 75 80
 Val Gly Asp Leu Leu Gly Val Val Gly Phe Pro Phe Gly Gly Ala Leu
 85 90 95
 Val Ser Phe Tyr Thr Asn Phe Leu Asn Thr Ile Trp Pro Ser Glu Asp
 100 105 110
 Pro Trp Lys Ala Phe Met Glu Gln Val Glu Ala Leu Met Asp Gln Lys
 115 120 125
 Ile Ala Asp Tyr Ala Lys Asn Lys Ala Leu Ala Glu Leu Gln Gly Leu
 130 135 140
 Gln Asn Asn Val Glu Asp Tyr Val Ser Ala Leu Ser Ser Trp Gln Lys
 145 150 155 160
 Asn Pro Val Ser Ser Arg Asn Pro His Ser Gln Gly Arg Ile Arg Glu
 165 170 175
 Leu Phe Ser Gln Ala Glu Ser His Phe Arg Asn Ser Met Pro Ser Phe
 180 185 190
 Ala Ile Ser Gly Tyr Glu Val Leu Phe Leu Thr Thr Tyr Ala Gln Ala
 195 200 205
 Ala Asn Thr His Leu Phe Leu Leu Lys Asp Ala Gln Ile Tyr Gly Glu
 210 215 220
 Glu Trp Gly Tyr Glu Lys Glu Asp Ile Ala Glu Phe Tyr Lys Arg Gln
 225 230 235 240
 Leu Lys Leu Thr Gln Glu Tyr Thr Asp His Cys Val Lys Trp Tyr Asn
 245 250 255
 Val Gly Leu Asp Lys Leu Arg Gly Ser Ser Tyr Glu Ser Trp Val Asn
 260 265 270
 Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu Ile
 275 280 285
 Ala Leu Phe Pro Leu Tyr Asp Val Arg Leu Tyr Pro Lys Glu Val Lys
 290 295 300
 Thr Glu Leu Thr Arg Asp Val Leu Thr Asp Pro Ile Val Gly Val Asn

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305          310          315          320
Asn Leu Arg Gly Tyr Gly Thr Thr Phe Ser Asn Ile Glu Asn Tyr Ile
          325          330          335
Arg Lys Pro His Leu Phe Asp Tyr Leu His Arg Ile Gln Phe His Thr
          340          345          350
Arg Phe Gln Pro Gly Tyr Tyr Gly Asn Asp Ser Phe Asn Tyr Trp Ser
          355          360          365
Gly Asn Tyr Val Ser Thr Arg Pro Ser Ile Gly Ser Asn Asp Ile Ile
          370          375          380
Thr Ser Pro Phe Tyr Gly Asn Lys Ser Ser Glu Pro Val Gln Asn Leu
385          390          395          400
Glu Phe Asn Gly Glu Lys Val Tyr Arg Ala Val Ala Asn Thr Asn Leu
          405          410          415
Ala Val Trp Pro Ser Ala Val Tyr Ser Gly Val Thr Lys Val Glu Phe
          420          425          430
Ser Gln Tyr Asn Asp Gln Thr Asp Glu Ala Ser Thr Gln Thr Tyr Asp
          435          440          445
Ser Lys Arg Asn Val Gly Ala Val Ser Trp Asp Ser Ile Asp Gln Leu
          450          455          460
Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Gly Tyr Ser His Gln
465          470          475          480
Leu Asn Tyr Val Met Cys Phe Leu Met Gln Gly Ser Arg Gly Thr Ile
          485          490          495
Pro Val Leu Thr Trp Thr His Lys Ser Val Asp Phe Phe Asn Met Ile
          500          505          510
Asp Ser Lys Lys Ile Thr Gln Leu Pro Leu Val Lys Ala Tyr Lys Leu
          515          520          525
Gln Ser Gly Ala Ser Val Val Ala Gly Pro Arg Phe Thr Gly Gly Asp
          530          535          540
Ile Ile Gln Cys Thr Glu Asn Gly Ser Ala Ala Thr Ile Tyr Val Thr
545          550          555          560
Pro Asp Val Ser Tyr Ser Gln Lys Tyr Arg Ala Arg Ile His Tyr Ala
          565          570          575
Ser Thr Ser Gln Ile Thr Phe Thr Leu Ser Leu Asp Gly Ala Pro Phe
          580          585          590
Asn Gln Tyr Tyr Phe Asp Lys Thr Ile Asn Lys Gly Asp Thr Leu Thr
          595          600          605
Tyr Asn Ser Phe Asn Leu Ala Ser Phe Ser Thr Pro Phe Glu Leu Ser
          610          615          620
Gly Asn Asn Leu Gln Ile Gly Val Thr Gly Leu Ser Ala Gly Asp Lys
625          630          635          640
Val Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Asn
          645          650

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<210> 36

<211> 659

<212> PRT

<213> *Bacillus thuringiensis*

<400> 36

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Met Ile Arg Met Gly Gly Arg Lys Met Asn Pro Asn Asn Arg Ser Glu
1          5          10          15
Tyr Asp Thr Ile Lys Val Thr Pro Asn Ser Glu Leu Pro Thr Asn His
          20          25          30
Asn Gln Tyr Pro Leu Ala Asp Asn Pro Asn Ser Thr Leu Glu Glu Leu
          35          40          45
Asn Tyr Lys Glu Phe Leu Arg Met Thr Ala Asp Asn Ser Thr Glu Val
          50          55          60
Leu Asp Ser Ser Thr Val Lys Asp Ala Val Gly Thr Gly Ile Ser Val
65          70          75          80
Val Gly Gln Ile Leu Gly Val Val Gly Val Pro Phe Ala Gly Ala Leu
          85          90          95
Thr Ser Phe Tyr Gln Ser Phe Leu Asn Ala Ile Trp Pro Ser Asp Ala
          100          105          110
Asp Pro Trp Lys Ala Phe Met Ala Gln Val Glu Val Leu Ile Asp Lys
          115          120          125
Lys Ile Glu Glu Tyr Ala Lys Ser Lys Ala Leu Ala Glu Leu Gln Gly

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130 135 140
 Leu Gln Asn Asn Phe Glu Asp Tyr Val Asn Ala Leu Asp Ser Trp Lys
 145 150 155 160
 Lys Ala Pro Val Asn Leu Arg Ser Arg Arg Ser Gln Asp Arg Ile Arg
 165 170 175
 Glu Leu Phe Ser Gln Ala Glu Ser His Phe Arg Asn Ser Met Pro Ser
 180 185 190
 Phe Ala Val Ser Lys Phe Glu Val Leu Phe Leu Pro Thr Tyr Ala Gln
 195 200 205
 Ala Ala Asn Thr His Leu Leu Leu Leu Lys Asp Ala Gln Val Phe Gly
 210 215 220
 Glu Glu Trp Gly Tyr Ser Ser Glu Asp Ile Ala Glu Phe Tyr Gln Arg
 225 230 235 240
 Gln Leu Lys Leu Thr Gln Gln Tyr Thr Asp His Cys Val Asn Trp Tyr
 245 250 255
 Asn Val Gly Leu Asn Ser Leu Arg Gly Ser Thr Tyr Asp Ala Trp Val
 260 265 270
 Lys Phe Asn Arg Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu
 275 280 285
 Ile Val Leu Phe Pro Phe Tyr Asp Val Arg Leu Tyr Ser Lys Gly Val
 290 295 300
 Lys Thr Glu Leu Thr Arg Asp Ile Phe Thr Asp Pro Ile Phe Thr Leu
 305 310 315 320
 Asn Ala Leu Gln Glu Tyr Gly Pro Thr Phe Ser Ser Ile Glu Asn Ser
 325 330 335
 Ile Arg Lys Pro His Leu Phe Asp Tyr Leu Arg Gly Ile Glu Phe His
 340 345 350
 Thr Arg Leu Arg Pro Gly Tyr Ser Gly Lys Asp Ser Phe Asn Tyr Trp
 355 360 365
 Ser Gly Asn Tyr Val Glu Thr Arg Pro Ser Ile Gly Ser Asn Asp Thr
 370 375 380
 Ile Thr Ser Pro Phe Tyr Gly Asp Lys Ser Ile Glu Pro Ile Gln Lys
 385 390 395 400
 Leu Ser Phe Asp Gly Gln Lys Val Tyr Arg Thr Ile Ala Asn Thr Asp
 405 410 415
 Ile Ala Ala Phe Pro Asp Gly Lys Ile Tyr Phe Gly Val Thr Lys Val
 420 425 430
 Asp Phe Ser Gln Tyr Asp Asp Gln Lys Asn Glu Thr Ser Thr Gln Thr
 435 440 445
 Tyr Asp Ser Lys Arg Tyr Asn Gly Tyr Leu Gly Ala Gln Asp Ser Ile
 450 455 460
 Asp Gln Leu Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Ala Tyr
 465 470 475 480
 Ser His Gln Leu Asn Tyr Ala Glu Cys Phe Leu Met Gln Asp Arg Arg
 485 490 495
 Gly Thr Ile Pro Phe Phe Thr Trp Thr His Arg Ser Val Asp Phe Phe
 500 505 510
 Asn Thr Ile Asp Ala Glu Lys Ile Thr Gln Leu Pro Val Val Lys Ala
 515 520 525
 Tyr Ala Leu Ser Ser Gly Ala Ser Ile Ile Glu Gly Pro Gly Phe Thr
 530 535 540
 Gly Gly Asn Leu Leu Phe Leu Lys Glu Ser Ser Asn Ser Ile Ala Lys
 545 550 555 560
 Phe Lys Val Thr Leu Asn Ser Ala Ala Leu Leu Gln Arg Tyr Arg Val
 565 570 575
 Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu Arg Leu Phe Val Gln Asn
 580 585 590
 Ser Asn Asn Asp Phe Leu Val Ile Tyr Ile Asn Lys Thr Met Asn Ile
 595 600 605
 Asp Gly Asp Leu Thr Tyr Gln Thr Phe Asp Phe Ala Thr Ser Asn Ser
 610 615 620
 Asn Met Gly Phe Ser Gly Asp Thr Asn Asp Phe Ile Ile Gly Ala Glu
 625 630 635 640
 Ser Phe Val Ser Asn Glu Lys Ile Tyr Ile Asp Lys Ile Glu Phe Ile
 645 650 655
 Pro Val Gln

<210> 37
 <211> 652
 <212> PRT
 <213> Bacillus thuringiensis

<400> 37
 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
 1 5 10 15
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
 20 25 30
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
 35 40 45
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
 50 55 60
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
 65 70 75 80
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
 85 90 95
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
 100 105 110
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
 115 120 125
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
 130 135 140
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
 145 150 155 160
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
 165 170 175
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
 180 185 190
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
 195 200 205
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
 210 215 220
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
 225 230 235 240
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
 245 250 255
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
 260 265 270
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
 275 280 285
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
 290 295 300
 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
 305 310 315 320
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
 325 330 335
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
 340 345 350
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
 355 360 365
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
 370 375 380
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
 385 390 395 400
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
 405 410 415
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
 420 425 430
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
 435 440 445
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
 450 455 460
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
 465 470 475 480
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp

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      485      490      495
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
      500      505      510
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
      515      520      525
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
      530      535      540
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
      545      550      555      560
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
      565      570      575
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
      580      585      590
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
      595      600      605
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
      610      615      620
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
      625      630      635      640
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
      645      650

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<210> 38
 <211> 1180
 <212> PRT
 <213> *Bacillus thuringiensis*

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<400> 38
Met Asn Pro Tyr Gln Asn Lys Asn Glu Tyr Glu Thr Leu Asn Ala Ser
  1      5      10      15
Gln Lys Lys Leu Asn Ile Ser Asn Asn Tyr Thr Arg Tyr Pro Ile Glu
  20      25      30
Asn Ser Pro Lys Gln Leu Leu Gln Ser Thr Asn Tyr Lys Asp Trp Leu
  35      40      45
Asn Met Cys Gln Gln Asn Gln Gln Tyr Gly Gly Asp Phe Glu Thr Phe
  50      55      60
Ile Asp Ser Gly Glu Leu Ser Ala Tyr Thr Ile Val Val Gly Thr Val
  65      70      75      80
Leu Thr Gly Phe Gly Phe Thr Thr Pro Leu Gly Leu Ala Leu Ile Gly
  85      90      95
Phe Gly Thr Leu Ile Pro Val Leu Phe Pro Ala Gln Asp Gln Ser Asn
  100      105      110
Thr Trp Ser Asp Phe Ile Thr Gln Thr Lys Asn Ile Ile Lys Lys Glu
  115      120      125
Ile Ala Ser Thr Tyr Ile Ser Asn Ala Asn Lys Ile Leu Asn Arg Ser
  130      135      140
Phe Asn Val Ile Ser Thr Tyr His Asn His Leu Lys Thr Trp Glu Asn
  145      150      155      160
Asn Pro Asn Pro Gln Asn Thr Gln Asp Val Arg Thr Gln Ile Gln Leu
  165      170      175
Val His Tyr His Phe Gln Asn Val Ile Pro Glu Leu Val Asn Ser Cys
  180      185      190
Pro Pro Asn Pro Ser Asp Cys Asp Tyr Tyr Asn Ile Leu Val Leu Ser
  195      200      205
Ser Tyr Ala Gln Ala Ala Asn Leu His Leu Thr Val Leu Asn Gln Ala
  210      215      220
Val Lys Phe Glu Ala Tyr Leu Lys Asn Asn Arg Gln Phe Asp Tyr Leu
  225      230      235      240
Glu Pro Leu Pro Thr Ala Ile Asp Tyr Tyr Pro Val Leu Thr Lys Ala
  245      250      255
Ile Glu Asp Tyr Thr Asn Tyr Cys Val Thr Thr Tyr Lys Lys Gly Leu
  260      265      270
Asn Leu Ile Lys Thr Thr Pro Asp Ser Asn Leu Asp Gly Asn Ile Asn
  275      280      285
Trp Asn Thr Tyr Asn Thr Tyr Arg Thr Lys Met Thr Thr Ala Val Leu
  290      295      300
Asp Leu Val Ala Leu Phe Pro Asn Tyr Asp Val Gly Lys Tyr Pro Ile

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- 71 -

850 855 860
 Glu Gly Ser Asn Arg Cys Glu Thr Ser Ala Val Pro Ala Asn Ile Gly
 865 870 875 880
 Asn Thr Ser Asp Met Leu Tyr Ser Cys Gln Tyr Asp Thr Gly Lys Lys
 885 890 895
 His Val Val Cys Gln Asp Ser His Gln Phe Ser Phe Thr Ile Asp Thr
 900 905 910
 Gly Ala Leu Asp Thr Asn Glu Asn Ile Gly Val Trp Val Met Phe Lys
 915 920 925
 Ile Ser Ser Pro Asp Gly Tyr Ala Ser Leu Asp Asn Leu Glu Val Ile
 930 935 940
 Glu Glu Gly Pro Ile Asp Gly Glu Ala Leu Ser Arg Val Lys His Met
 945 950 955 960
 Glu Lys Lys Trp Asn Asp Gln Met Glu Ala Lys Arg Ser Glu Thr Gln
 965 970 975
 Gln Ala Tyr Asp Val Ala Lys Gln Ala Ile Asp Ala Leu Phe Thr Asn
 980 985 990
 Val Gln Asp Glu Ala Leu Gln Phe Asp Thr Thr Leu Ala Gln Ile Gln
 995 1000 1005
 Tyr Ala Glu Tyr Leu Val Gln Ser Ile Pro Tyr Val Tyr Asn Asp Trp
 1010 1015 1020
 Leu Ser Asp Val Pro Gly Met Asn Tyr Asp Ile Tyr Val Glu Leu Asp
 1025 1030 1035 1040
 Ala Arg Val Ala Gln Ala Arg Tyr Leu Tyr Asp Thr Arg Asn Ile Ile
 1045 1050 1055
 Lys Asn Gly Asp Phe Thr Gln Gly Val Met Gly Trp His Val Thr Gly
 1060 1065 1070
 Asn Ala Asp Val Gln Gln Ile Asp Gly Val Ser Val Leu Val Leu Ser
 1075 1080 1085
 Asn Trp Ser Ala Gly Val Ser Gln Asn Val His Leu Gln His Asn His
 1090 1095 1100
 Gly Tyr Val Leu Arg Val Ile Ala Lys Lys Glu Gly Pro Gly Asn Gly
 1105 1110 1115 1120
 Tyr Val Thr Leu Met Asp Cys Glu Glu Asn Gln Glu Lys Leu Thr Phe
 1125 1130 1135
 Thr Ser Cys Glu Glu Gly Tyr Ile Thr Lys Thr Val Asp Val Phe Pro
 1140 1145 1150
 Asp Thr Asp Arg Val Arg Ile Glu Ile Gly Glu Thr Glu Gly Ser Phe
 1155 1160 1165
 Tyr Ile Glu Ser Ile Glu Leu Ile Cys Met Asn Glu
 1170 1175 1180

<210> 39

<211> 1136

<212> PRT

<213> *Bacillus thuringiensis*

<400> 39

Met Asn Ser Gly Tyr Pro Leu Ala Asn Asp Leu Gln Gly Ser Met Lys
 1 5 10 15
 Asn Thr Asn Tyr Lys Asp Trp Leu Ala Met Cys Glu Asn Asn Gln Gln
 20 25 30
 Tyr Gly Val Asn Pro Ala Ala Ile Asn Ser Ser Ser Val Ser Thr Ala
 35 40 45
 Leu Lys Val Ala Gly Ala Ile Leu Lys Phe Val Asn Pro Pro Ala Gly
 50 55 60
 Thr Val Leu Thr Val Leu Ser Ala Val Leu Pro Ile Leu Trp Pro Thr
 65 70 75 80
 Asn Thr Pro Thr Pro Glu Arg Val Trp Asn Asp Phe Met Thr Asn Thr
 85 90 95
 Gly Asn Leu Ile Asp Gln Thr Val Thr Ala Tyr Val Arg Thr Asp Ala
 100 105 110
 Asn Ala Lys Met Thr Val Val Lys Asp Tyr Leu Asp Gln Tyr Thr Thr
 115 120 125
 Lys Phe Asn Thr Trp Lys Arg Glu Pro Asn Asn Gln Ser Tyr Arg Thr
 130 135 140
 Ala Val Ile Thr Gln Phe Asn Leu Thr Ser Ala Lys Leu Arg Glu Thr

145					150					155					160
Ala	Val	Tyr	Phe	Ser	Asn	Leu	Val	Gly	Tyr	Glu	Leu	Leu	Leu	Leu	Pro
				165					170					175	
Ile	Tyr	Ala	Gln	Val	Ala	Asn	Phe	Asn	Leu	Leu	Leu	Ile	Arg	Asp	Gly
			180					185					190		
Leu	Ile	Asn	Ala	Gln	Glu	Trp	Ser	Leu	Ala	Arg	Ser	Ala	Gly	Asp	Gln
		195					200					205			
Leu	Tyr	Asn	Thr	Met	Val	Gln	Tyr	Thr	Lys	Glu	Tyr	Ile	Ala	His	Ser
	210					215					220				
Ile	Thr	Trp	Tyr	Asn	Lys	Gly	Leu	Asp	Val	Leu	Arg	Asn	Lys	Ser	Asn
225				230						235				240	
Gly	Gln	Trp	Ile	Thr	Phe	Asn	Asp	Tyr	Lys	Arg	Glu	Met	Thr	Ile	Gln
				245					250					255	
Val	Leu	Asp	Ile	Leu	Ala	Leu	Phe	Ala	Ser	Tyr	Asp	Pro	Arg	Arg	Tyr
		260						265					270		
Pro	Ala	Asp	Lys	Ile	Asp	Asn	Thr	Lys	Leu	Ser	Lys	Thr	Glu	Phe	Thr
		275					280					285			
Arg	Glu	Ile	Tyr	Thr	Ala	Leu	Val	Glu	Ser	Pro	Ser	Ser	Lys	Ser	Ile
	290					295					300				
Ala	Ala	Leu	Glu	Ala	Ala	Leu	Thr	Arg	Asp	Val	His	Leu	Phe	Thr	Trp
305					310					315				320	
Leu	Lys	Arg	Val	Asp	Phe	Trp	Thr	Asn	Thr	Ile	Tyr	Gln	Asp	Leu	Arg
				325					330					335	
Phe	Leu	Ser	Ala	Asn	Lys	Ile	Gly	Phe	Ser	Tyr	Thr	Asn	Ser	Ser	Ala
		340					345					350			
Met	Gln	Glu	Ser	Gly	Ile	Tyr	Gly	Ser	Ser	Gly	Phe	Gly	Ser	Asn	Leu
	355						360					365			
Thr	His	Gln	Ile	Gln	Leu	Asn	Ser	Asn	Val	Tyr	Lys	Thr	Ser	Ile	Thr
	370					375					380				
Asp	Thr	Ser	Ser	Pro	Ser	Asn	Arg	Val	Thr	Lys	Met	Asp	Phe	Tyr	Lys
385				390						395				400	
Ile	Asp	Gly	Thr	Leu	Ala	Ser	Tyr	Asn	Ser	Asn	Ile	Thr	Pro	Thr	Pro
			405						410					415	
Glu	Gly	Leu	Arg	Thr	Thr	Phe	Phe	Gly	Phe	Ser	Thr	Asn	Glu	Asn	Thr
		420						425				430			
Pro	Asn	Gln	Pro	Thr	Val	Asn	Asp	Tyr	Thr	His	Ile	Leu	Ser	Tyr	Ile
	435						440				445				
Lys	Thr	Asp	Val	Ile	Asp	Tyr	Asn	Ser	Asn	Arg	Val	Ser	Phe	Ala	Trp
	450					455					460				
Thr	His	Lys	Ile	Val	Asp	Pro	Asn	Asn	Gln	Ile	Tyr	Thr	Asp	Ala	Ile
465					470					475				480	
Thr	Gln	Val	Pro	Ala	Val	Lys	Ser	Asn	Phe	Leu	Asn	Ala	Thr	Ala	Lys
			485						490				495		
Val	Ile	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Val	Ala	Leu	Thr
		500						505					510		
Ser	Asn	Gly	Thr	Leu	Ser	Gly	Arg	Met	Glu	Ile	Gln	Cys	Lys	Thr	Ser
	515						520					525			
Ile	Phe	Asn	Asp	Pro	Thr	Arg	Ser	Tyr	Gly	Leu	Arg	Ile	Arg	Tyr	Ala
	530					535					540				
Ala	Asn	Ser	Pro	Ile	Val	Leu	Asn	Val	Ser	Tyr	Val	Leu	Gln	Gly	Val
545				550						555				560	
Ser	Arg	Gly	Thr	Thr	Ile	Ser	Thr	Glu	Ser	Thr	Phe	Ser	Arg	Pro	Asn
			565						570					575	
Asn	Ile	Ile	Pro	Thr	Asp	Leu	Lys	Tyr	Glu	Glu	Phe	Arg	Tyr	Lys	Asp
		580						585					590		
Pro	Phe	Asp	Ala	Ile	Val	Pro	Met	Arg	Leu	Ser	Ser	Asn	Gln	Leu	Ile
	595						600					605			
Thr	Ile	Ala	Ile	Gln	Pro	Leu	Asn	Met	Thr	Ser	Asn	Asn	Gln	Val	Ile
	610					615					620				
Ile	Asp	Arg	Ile	Glu	Ile	Ile	Pro	Ile	Thr	Gln	Ser	Val	Leu	Asp	Glu
625					630					635				640	
Thr	Glu	Asn	Gln	Asn	Leu	Glu	Ser	Glu	Arg	Glu	Val	Val	Asn	Ala	Leu
			645						650					655	
Phe	Thr	Asn	Asp	Ala	Lys	Asp	Ala	Leu	Asn	Ile	Gly	Thr	Thr	Asp	Tyr
		660						665				670			
Asp	Ile	Asp	Gln	Ala	Ala	Asn	Leu	Val	Glu	Cys	Ile	Ser	Glu	Glu	Leu
	675					680					685				
Tyr	Pro	Lys	Glu	Lys	Met	Leu	Leu	Leu	Asp	Glu	Val	Lys	Asn	Ala	Lys

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        690                695                700
Gln Leu Ser Gln Ser Arg Asn Val Leu Gln Asn Gly Asp Phe Glu Ser
705                710                715                720
Ala Thr Leu Gly Trp Thr Thr Ser Asp Asn Ile Thr Ile Gln Glu Asp
        725                730                735
Asp Pro Ile Phe Lys Gly His Tyr Leu His Met Ser Gly Ala Arg Asp
        740                745                750
Ile Asp Gly Thr Ile Phe Pro Thr Tyr Ile Phe Gln Lys Ile Asp Glu
        755                760                765
Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Leu Val Arg Gly Phe Val Gly
        770                775                780
Ser Ser Lys Asp Val Glu Leu Val Val Ser Arg Tyr Gly Glu Glu Ile
785                790                795                800
Asp Ala Ile Met Asn Val Pro Ala Asp Leu Asn Tyr Leu Tyr Pro Ser
        805                810                815
Thr Phe Asp Cys Glu Gly Ser Asn Arg Cys Glu Thr Ser Ala Val Pro
        820                825                830
Ala Asn Ile Gly Asn Thr Ser Asp Met Leu Tyr Ser Cys Gln Tyr Asp
        835                840                845
Thr Gly Lys Lys His Val Val Cys Gln Asp Ser His Gln Phe Ser Phe
        850                855                860
Thr Ile Asp Thr Gly Ala Leu Asp Thr Asn Glu Asn Ile Gly Val Trp
865                870                875                880
Val Met Phe Lys Ile Ser Ser Pro Asp Gly Tyr Ala Ser Leu Asp Asn
        885                890                895
Leu Glu Val Ile Glu Glu Gly Pro Ile Asp Gly Glu Ala Leu Ser Arg
        900                905                910
Val Lys His Met Glu Lys Lys Trp Asn Asp Gln Met Glu Ala Lys Arg
        915                920                925
Ser Glu Thr Gln Gln Ala Tyr Asp Val Ala Lys Gln Ala Ile Asp Ala
        930                935                940
Leu Phe Thr Asn Val Gln Asp Glu Ala Leu Gln Phe Asp Thr Thr Leu
945                950                955                960
Ala Gln Ile Gln Tyr Ala Glu Tyr Leu Val Gln Ser Ile Pro Tyr Val
        965                970                975
Tyr Asn Asp Trp Leu Ser Asp Val Pro Gly Met Asn Tyr Asp Ile Tyr
        980                985                990
Val Glu Leu Asp Ala Arg Val Ala Gln Ala Arg Tyr Leu Tyr Asp Thr
        995                1000                1005
Arg Asn Ile Ile Lys Asn Gly Asp Phe Thr Gln Gly Val Met Gly Trp
        1010                1015                1020
His Val Thr Gly Asn Ala Asp Val Gln Gln Ile Asp Gly Val Ser Val
1025                1030                1035                1040
Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln Asn Val His Leu
        1045                1050                1055
Gln His Asn His Gly Tyr Val Leu Arg Val Ile Ala Lys Lys Glu Gly
        1060                1065                1070
Pro Gly Asn Gly Tyr Val Thr Leu Met Asp Cys Glu Glu Asn Gln Glu
        1075                1080                1085
Lys Leu Thr Phe Thr Ser Cys Glu Glu Gly Tyr Ile Thr Lys Thr Val
        1090                1095                1100
Asp Val Phe Pro Asp Thr Asp Arg Val Arg Ile Glu Ile Gly Glu Thr
1105                1110                1115                1120
Glu Gly Ser Phe Tyr Ile Glu Ser Ile Glu Leu Ile Cys Met Asn Glu
        1125                1130                1135

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<210> 40

<211> 475

<212> PRT

<213> Bacillus thuringiensis

<400> 40

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Met Ile Ile Asp Ser Lys Thr Thr Leu Pro Arg His Ser Leu Ile His
 1                5                10                15
Thr Ile Lys Leu Asn Ser Asn Lys Lys Tyr Gly Pro Gly Asp Met Thr
        20                25                30
Asn Gly Asn Gln Phe Ile Ile Ser Lys Gln Glu Trp Ala Thr Ile Gly

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      35      40      45
Ala Tyr Ile Gln Thr Gly Leu Gly Leu Pro Val Asn Glu Gln Gln Leu
  50      55      60
Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser Ile Pro Ser Asp Phe
  65      70      75      80
Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys Thr Ser Ala Glu Trp
      85      90      95
Trp Asn Lys Asn Leu Tyr Pro Leu Ile Ile Lys Ser Ala Asn Asp Ile
      100      105      110
Ala Ser Tyr Gly Phe Lys Val Ala Gly Asp Pro Ser Ile Lys Lys Asp
      115      120      125
Gly Tyr Phe Lys Lys Leu Gln Asp Glu Leu Asp Asn Ile Val Asp Asn
      130      135      140
Asn Ser Asp Asp Asp Ala Ile Ala Lys Ala Ile Lys Asp Phe Lys Ala
  145      150      155      160
Arg Cys Gly Ile Leu Ile Lys Glu Ala Lys Gln Tyr Glu Glu Ala Ala
      165      170      175
Lys Asn Ile Val Thr Ser Leu Asp Gln Phe Leu His Gly Asp Gln Lys
      180      185      190
Lys Leu Glu Gly Val Ile Asn Ile Gln Lys Arg Leu Lys Glu Val Gln
      195      200      205
Thr Ala Leu Asn Gln Ala His Gly Glu Ser Ser Pro Ala His Lys Glu
      210      215      220
Leu Leu Glu Lys Val Lys Asn Leu Lys Thr Thr Leu Glu Arg Thr Ile
  225      230      235      240
Lys Ala Glu Gln Asp Leu Glu Lys Lys Val Glu Tyr Ser Phe Leu Leu
      245      250      255
Gly Pro Leu Leu Gly Phe Val Val Tyr Glu Ile Leu Glu Asn Thr Ala
      260      265      270
Val Gln His Ile Lys Asn Gln Ile Asp Glu Ile Lys Lys Gln Leu Asp
      275      280      285
Ser Ala Gln His Asp Leu Asp Arg Asp Val Lys Ile Ile Gly Met Leu
  290      295      300
Asn Ser Ile Asn Thr Asp Ile Asp Asn Leu Tyr Ser Gln Gly Gln Glu
  305      310      315      320
Ala Ile Lys Val Phe Gln Lys Leu Gln Gly Ile Trp Ala Thr Ile Gly
      325      330      335
Ala Gln Ile Glu Asn Leu Arg Thr Thr Ser Leu Gln Glu Val Gln Asp
      340      345      350
Ser Asp Asp Ala Asp Glu Ile Gln Ile Glu Leu Glu Asp Ala Ser Asp
      355      360      365
Ala Trp Leu Val Val Ala Gln Glu Ala Arg Asp Phe Thr Leu Asn Ala
  370      375      380
Tyr Ser Thr Asn Ser Arg Gln Asn Leu Pro Ile Asn Val Ile Ser Asp
  385      390      395      400
Ser Cys Asn Cys Ser Thr Thr Asn Met Thr Ser Asn Gln Tyr Ser Asn
      405      410      415
Pro Thr Thr Asn Met Thr Ser Asn Gln Tyr Met Ile Ser His Glu Tyr
      420      425      430
Thr Ser Leu Pro Asn Asn Phe Met Leu Ser Arg Asn Ser Asn Leu Glu
      435      440      445
Tyr Lys Cys Pro Glu Asn Asn Phe Met Ile Tyr Trp Tyr Asn Asn Ser
  450      455      460
Asp Trp Tyr Asn Asn Ser Asp Trp Tyr Asn Asn
  465      470      475

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<210> 41

<211> 1138

<212> PRT

<213> Bacillus thuringiensis

<400> 41

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Met Asn Leu Asn Asn Leu Asp Gly Tyr Glu Asp Ser Asn Arg Thr Leu
  1      5      10      15
Asn Asn Ser Leu Asn Tyr Pro Thr Gln Lys Ala Leu Ser Pro Ser Leu
      20      25      30
Lys Asn Met Asn Tyr Gln Asp Phe Leu Ser Ile Thr Glu Arg Glu Gln

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      35      40      45
Pro Glu Ala Leu Ala Ser Gly Asn Thr Ala Ile Asn Thr Val Val Ser
  50      55      60
Val Thr Gly Ala Thr Leu Ser Ala Leu Gly Val Pro Gly Ala Ser Phe
  65      70      75      80
Ile Thr Asn Phe Tyr Leu Lys Ile Ala Gly Leu Leu Trp Pro Glu Asn
      85      90      95
Gly Lys Ile Trp Asp Glu Phe Met Thr Glu Val Glu Ala Leu Ile Asp
      100      105      110
Gln Lys Ile Glu Glu Tyr Val Arg Asn Lys Ala Ile Ala Glu Leu Asp
      115      120      125
Gly Leu Gly Ser Ala Leu Asp Lys Tyr Gln Lys Ala Leu Ala Asp Trp
      130      135      140
Leu Gly Lys Gln Asp Asp Pro Glu Ala Ile Leu Ser Val Ala Thr Glu
      145      150      155      160
Phe Arg Ile Ile Asp Ser Leu Phe Glu Phe Ser Met Pro Ser Phe Lys
      165      170      175
Val Thr Gly Tyr Glu Ile Pro Leu Leu Thr Val Tyr Ala Gln Ala Ala
      180      185      190
Asn Leu His Leu Ala Leu Leu Arg Asp Ser Thr Leu Tyr Gly Asp Lys
      195      200      205
Trp Gly Phe Thr Gln Asn Asn Ile Glu Glu Asn Tyr Asn Arg Gln Lys
      210      215      220
Lys Arg Ile Ser Glu Tyr Ser Asp His Cys Thr Lys Trp Tyr Asn Ser
      225      230      235      240
Gly Leu Ser Arg Leu Asn Gly Ser Thr Tyr Glu Gln Trp Ile Asn Tyr
      245      250      255
Asn Arg Phe Arg Arg Glu Met Ile Leu Met Ala Leu Asp Leu Val Ala
      260      265      270
Val Phe Pro Phe His Asp Pro Arg Arg Tyr Ser Met Glu Thr Ser Thr
      275      280      285
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ser Leu Ser Ile Ser
      290      295      300
Asn Pro Asp Ile Gly Pro Ser Phe Ser Gln Met Glu Asn Thr Ala Ile
      305      310      315      320
Arg Thr Pro His Leu Val Asp Tyr Leu Asp Glu Leu Tyr Ile Tyr Thr
      325      330      335
Ser Lys Tyr Lys Ala Phe Ser His Glu Ile Gln Pro Asp Leu Phe Tyr
      340      345      350
Trp Ser Ala His Lys Val Ser Phe Lys Lys Ser Glu Gln Ser Asn Leu
      355      360      365
Tyr Thr Thr Gly Ile Tyr Gly Lys Thr Ser Gly Tyr Ile Ser Ser Gly
      370      375      380
Ala Tyr Ser Phe His Gly Asn Asp Ile Tyr Arg Thr Leu Ala Ala Pro
      385      390      395      400
Ser Val Val Val Tyr Pro Tyr Thr Gln Asn Tyr Gly Val Glu Gln Val
      405      410      415
Glu Phe Tyr Gly Val Lys Gly His Val His Tyr Arg Gly Asp Asn Lys
      420      425      430
Tyr Asp Leu Thr Tyr Asp Ser Ile Asp Gln Leu Pro Pro Asp Gly Glu
      435      440      445
Pro Ile His Glu Lys Tyr Thr His Arg Leu Cys His Ala Thr Ala Ile
      450      455      460
Phe Lys Ser Thr Pro Asp Tyr Asp Asn Ala Thr Ile Pro Ile Phe Ser
      465      470      475      480
Trp Thr His Arg Ser Ala Glu Tyr Tyr Asn Arg Ile Tyr Pro Asn Lys
      485      490      495
Ile Thr Lys Ile Pro Ala Val Lys Met Tyr Lys Leu Asp Asp Pro Ser
      500      505      510
Thr Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Leu Val Lys Arg
      515      520      525
Gly Ser Thr Gly Tyr Ile Gly Asp Ile Lys Ala Thr Val Asn Ser Pro
      530      535      540
Leu Ser Gln Lys Tyr Arg Val Arg Val Arg Tyr Ala Thr Asn Val Ser
      545      550      555      560
Gly Gln Phe Asn Val Tyr Ile Asn Asp Lys Ile Thr Leu Gln Thr Lys
      565      570      575
Phe Gln Asn Thr Val Glu Thr Ile Gly Glu Gly Lys Asp Leu Thr Tyr

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580 585 590
 Gly Ser Phe Gly Tyr Ile Glu Tyr Ser Thr Thr Ile Gln Phe Pro Asp
 595 600 605
 Glu His Pro Lys Ile Thr Leu His Leu Ser Asp Leu Ser Asn Asn Ser
 610 615 620
 Ser Phe Tyr Val Asp Ser Ile Glu Phe Ile Pro Val Asp Val Asn Tyr
 625 630 635 640
 Ala Glu Lys Glu Lys Leu Glu Lys Ala Gln Lys Ala Val Asn Thr Leu
 645 650 655
 Phe Thr Glu Gly Arg Asn Ala Leu Gln Lys Asp Val Thr Asp Tyr Lys
 660 665 670
 Val Asp Gln Val Ser Ile Leu Val Asp Cys Ile Ser Gly Asp Leu Tyr
 675 680 685
 Pro Asn Glu Lys Arg Glu Leu Gln Asn Leu Val Lys Tyr Ala Lys Arg
 690 695 700
 Leu Ser Tyr Ser Arg Asn Leu Leu Leu Asp Pro Thr Phe Asp Ser Ile
 705 710 715 720
 Asn Ser Ser Glu Glu Asn Gly Trp Tyr Gly Ser Asn Gly Ile Val Ile
 725 730 735
 Gly Asn Gly Asp Phe Val Phe Lys Gly Asn Tyr Leu Ile Phe Ser Gly
 740 745 750
 Thr Asn Asp Thr Gln Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
 755 760 765
 Ser Lys Leu Lys Glu Tyr Thr Arg Tyr Lys Leu Lys Gly Phe Ile Glu
 770 775 780
 Ser Ser Gln Asp Leu Glu Ala Tyr Val Ile Arg Tyr Asp Ala Lys His
 785 790 795 800
 Arg Thr Leu Asp Val Ser Asp Asn Leu Leu Pro Asp Ile Leu Pro Glu
 805 810 815
 Asn Thr Cys Gly Glu Pro Asn Arg Cys Ala Ala Gln Gln Tyr Leu Asp
 820 825 830
 Glu Asn Pro Ser Pro Glu Cys Ser Ser Met Gln Asp Gly Ile Leu Ser
 835 840 845
 Asp Ser His Ser Phe Ser Leu Asn Ile Asp Thr Gly Ser Ile Asn His
 850 855 860
 Asn Glu Asn Leu Gly Ile Trp Val Leu Phe Lys Ile Ser Thr Leu Glu
 865 870 875 880
 Gly Tyr Ala Lys Phe Gly Asn Leu Glu Val Ile Glu Asp Gly Pro Val
 885 890 895
 Ile Gly Glu Ala Leu Ala Arg Val Lys Arg Gln Glu Thr Lys Trp Arg
 900 905 910
 Asn Lys Leu Ala Gln Leu Thr Thr Glu Thr Gln Ala Ile Tyr Thr Arg
 915 920 925
 Ala Lys Gln Ala Leu Asp Asn Leu Phe Ala Asn Ala Gln Asp Ser His
 930 935 940
 Leu Lys Arg Asp Val Thr Phe Ala Glu Ile Ala Ala Ala Arg Lys Ile
 945 950 955 960
 Val Gln Ser Ile Arg Glu Ala Tyr Met Ser Trp Leu Ser Val Val Pro
 965 970 975
 Gly Val Asn His Pro Ile Phe Thr Glu Leu Ser Gly Arg Val Gln Arg
 980 985 990
 Ala Phe Gln Leu Tyr Asp Val Arg Asn Val Val Arg Asn Gly Arg Phe
 995 1000 1005
 Leu Asn Gly Leu Ser Asp Trp Ile Val Thr Ser Asp Val Lys Val Gln
 1010 1015 1020
 Glu Glu Asn Gly Asn Asn Val Leu Val Leu Asn Asn Trp Asp Ala Gln
 1025 1030 1035 1040
 Val Leu Gln Asn Val Lys Leu Tyr Gln Asp Arg Gly Tyr Ile Leu His
 1045 1050 1055
 Val Thr Ala Arg Lys Ile Gly Ile Gly Glu Gly Tyr Ile Thr Ile Thr
 1060 1065 1070
 Asp Glu Glu Gly His Thr Asp Gln Leu Arg Phe Thr Ala Cys Glu Glu
 1075 1080 1085
 Ile Asp Ala Ser Asn Ala Phe Ile Ser Gly Tyr Ile Thr Lys Glu Leu
 1090 1095 1100
 Glu Phe Phe Pro Asp Thr Glu Lys Val His Ile Glu Ile Gly Glu Thr
 1105 1110 1115 1120
 Glu Gly Ile Phe Leu Val Glu Ser Ile Glu Leu Phe Leu Met Glu Glu

Leu Cys 1125 1130 1135

 <210> 42
 <211> 1157
 <212> PRT
 <213> *Bacillus thuringiensis*

 <400> 42
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 Ser Thr Ser Val Ser Ser Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 Pro Thr Asp Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 Ser Gly Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile
 50 55 60
 Ser Ser Ser Thr Ile Gln Thr Gly Ile Gly Ile Val Gly Arg Ile Leu
 65 70 75 80
 Gly Ala Leu Gly Val Pro Phe Ala Ser Gln Ile Ala Ser Phe Tyr Ser
 85 90 95
 Phe Ile Val Gly Gln Leu Trp Pro Ser Lys Ser Val Asp Ile Trp Gly
 100 105 110
 Glu Ile Met Glu Arg Val Glu Glu Leu Val Asp Gln Lys Ile Glu Lys
 115 120 125
 Tyr Val Lys Asp Lys Ala Leu Ala Glu Leu Lys Gly Leu Gly Asn Ala
 130 135 140
 Leu Asp Val Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn Arg Asn
 145 150 155 160
 Asp Ala Arg Thr Arg Ser Val Val Ser Asn Gln Phe Ile Ala Leu Asp
 165 170 175
 Leu Asn Phe Val Ser Ser Ile Pro Ser Phe Ala Val Ser Gly His Glu
 180 185 190
 Val Leu Leu Leu Ala Val Tyr Ala Gln Ala Val Asn Leu His Leu Leu
 195 200 205
 Leu Leu Arg Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Phe Thr Pro
 210 215 220
 Gly Glu Ile Ser Arg Phe Tyr Asn Arg Gln Val Gln Leu Thr Ala Glu
 225 230 235 240
 Tyr Ser Asp Tyr Cys Val Lys Trp Tyr Lys Ile Gly Leu Asp Lys Leu
 245 250 255
 Lys Gly Thr Thr Ser Lys Ser Trp Leu Asn Tyr His Gln Phe Arg Arg
 260 265 270
 Glu Met Thr Leu Leu Val Leu Asp Leu Val Ala Leu Phe Pro Asn Tyr
 275 280 285
 Asp Thr His Met Tyr Pro Ile Glu Thr Thr Ala Gln Leu Thr Arg Asp
 290 295 300
 Val Tyr Thr Asp Pro Ile Ala Phe Asn Ile Val Thr Ser Thr Gly Phe
 305 310 315 320
 Cys Asn Pro Trp Ser Thr His Ser Gly Ile Leu Phe Tyr Glu Val Glu
 325 330 335
 Asn Asn Val Ile Arg Pro Pro His Leu Phe Asp Ile Leu Ser Ser Val
 340 345 350
 Glu Ile Asn Thr Ser Arg Gly Gly Ile Thr Leu Asn Asn Asp Ala Tyr
 355 360 365
 Ile Asn Tyr Trp Ser Gly His Thr Leu Lys Tyr Arg Arg Thr Ala Asp
 370 375 380
 Ser Thr Val Thr Tyr Thr Ala Asn Tyr Gly Arg Ile Thr Ser Glu Lys
 385 390 395 400
 Asn Ser Phe Ala Leu Glu Asp Arg Asp Ile Phe Glu Ile Asn Ser Thr
 405 410 415
 Val Ala Asn Leu Ala Asn Tyr Tyr Gln Lys Ala Tyr Gly Val Pro Gly
 420 425 430
 Ser Trp Phe His Met Val Lys Arg Gly Thr Ser Ser Thr Thr Ala Tyr
 435 440 445
 Leu Tyr Ser Lys Thr His Thr Ala Leu Gln Gly Cys Thr Gln Val Tyr

450 455 460
 Glu Ser Ser Asp Glu Ile Pro Leu Asp Arg Thr Val Pro Val Ala Glu
 465 470 475 480
 Ser Tyr Ser His Arg Leu Ser His Ile Thr Ser His Ser Phe Ser Lys
 485 490 495
 Asn Gly Ser Ala Tyr Tyr Gly Ser Phe Pro Val Phe Val Trp Thr His
 500 505 510
 Thr Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln
 515 520 525
 Ile Pro Ala Val Lys Gly Asp Met Leu Tyr Leu Gly Gly Ser Val Val
 530 535 540
 Gln Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Lys Arg Thr Asn Pro
 545 550 555 560
 Ser Ile Leu Gly Thr Phe Ala Val Thr Val Asn Gly Ser Leu Ser Gln
 565 570 575
 Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Phe Glu Phe
 580 585 590
 Thr Leu Tyr Leu Gly Asp Thr Ile Glu Lys Asn Arg Phe Asn Lys Thr
 595 600 605
 Met Asp Asn Gly Ala Ser Leu Thr Tyr Glu Thr Phe Lys Phe Ala Ser
 610 615 620
 Phe Ile Thr Asp Phe Gln Phe Arg Glu Thr Gln Asp Lys Ile Leu Leu
 625 630 635 640
 Ser Met Gly Asp Phe Ser Ser Gly Gln Glu Val Tyr Ile Asp Arg Ile
 645 650 655
 Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu Gln Asp Leu Glu
 660 665 670
 Ala Ala Lys Lys Ala Val Asn Ala Leu Phe Thr Asn Thr Lys Asp Gly
 675 680 685
 Leu Arg Pro Gly Val Thr Asp Tyr Glu Val Asn Gln Ala Ala Asn Leu
 690 695 700
 Val Glu Cys Leu Ser Asp Leu Tyr Pro Asn Glu Lys Arg Leu Leu
 705 710 715 720
 Phe Asp Ala Val Arg Glu Ala Lys Arg Leu Ser Gly Ala Arg Asn Leu
 725 730 735
 Leu Gln Asp Pro Asp Phe Gln Glu Ile Asn Gly Glu Asn Gly Trp Ala
 740 745 750
 Ala Ser Thr Gly Ile Glu Ile Val Glu Gly Asp Ala Val Phe Lys Gly
 755 760 765
 Arg Tyr Leu Arg Leu Pro Gly Ala Arg Glu Ile Asp Thr Glu Thr Tyr
 770 775 780
 Pro Thr Tyr Leu Tyr Gln Lys Val Glu Glu Gly Val Leu Lys Pro Tyr
 785 790 795 800
 Thr Arg Tyr Arg Leu Arg Gly Phe Val Gly Ser Ser Gln Gly Leu Glu
 805 810 815
 Ile Tyr Thr Ile Arg His Gln Thr Asn Arg Ile Val Lys Asn Val Pro
 820 825 830
 Asp Asp Leu Leu Pro Asp Val Ser Pro Val Asn Ser Asp Gly Ser Ile
 835 840 845
 Asn Arg Cys Ser Glu Gln Lys Tyr Val Asn Ser Arg Leu Glu Gly Glu
 850 855 860
 Asn Arg Ser Gly Asp Ala His Glu Phe Ser Leu Pro Ile Asp Ile Gly
 865 870 875 880
 Glu Leu Asp Tyr Asn Glu Asn Ala Gly Ile Trp Val Gly Phe Lys Ile
 885 890 895
 Thr Asp Pro Glu Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val Glu
 900 905 910
 Glu Gly Pro Leu Ser Gly Asp Ala Leu Glu Arg Leu Gln Arg Glu Glu
 915 920 925
 Gln Gln Trp Lys Ile Gln Met Thr Arg Arg Arg Glu Glu Thr Asp Arg
 930 935 940
 Arg Tyr Met Ala Ser Lys Gln Ala Val Asp Arg Leu Tyr Ala Asp Tyr
 945 950 955 960
 Gln Asp Gln Gln Leu Asn Pro Asp Val Glu Ile Thr Asp Leu Thr Ala
 965 970 975
 Ala Gln Asp Leu Ile Gln Ser Ile Pro Tyr Val Tyr Asn Glu Met Phe
 980 985 990
 Pro Glu Ile Pro Gly Met Asn Tyr Thr Lys Phe Thr Glu Leu Thr Asp

995 1000 1005
 Arg Leu Gln Gln Ala Trp Asn Leu Tyr Asp Gln Arg Asn Ala Ile Pro
 1010 1015 1020
 Asn Gly Asp Phe Arg Asn Gly Leu Ser Asn Trp Asn Ala Thr Pro Gly
 1025 1030 1035 1040
 Val Glu Val Gln Gln Ile Asn His Thr Ser Val Leu Val Ile Pro Asn
 1045 1050 1055
 Trp Asp Glu Gln Val Ser Gln Gln Phe Thr Val Gln Pro Asn Gln Arg
 1060 1065 1070
 Tyr Val Leu Arg Val Thr Ala Arg Lys Glu Gly Val Gly Asn Gly Tyr
 1075 1080 1085
 Val Ser Ile Arg Asp Gly Gly Asn Gln Ser Glu Thr Leu Thr Phe Ser
 1090 1095 1100
 Ala Ser Asp Tyr Asp Thr Asn Gly Val Tyr Asn Asp Gln Thr Gly Tyr
 1105 1110 1115 1120
 Ile Thr Lys Thr Val Thr Phe Ile Pro Tyr Thr Asp Gln Met Trp Ile
 1125 1130 1135
 Glu Ile Ser Glu Thr Glu Gly Thr Phe Tyr Ile Glu Ser Val Glu Leu
 1140 1145 1150
 Ile Val Asp Val Glu
 1155

<210> 43
 <211> 675
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 43
 Met Asn Pro Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Phe Asn Ala Pro
 1 5 10 15
 Ser Asn Gly Phe Ser Lys Ser Asn Asn Tyr Ser Arg Tyr Pro Leu Ala
 20 25 30
 Asn Lys Pro Asn Gln Pro Leu Lys Asn Thr Asn Tyr Lys Asp Trp Leu
 35 40 45
 Asn Val Cys Gln Asp Asn Gln Tyr Gly Asn Asn Ala Gly Asn Phe
 50 55 60
 Ala Ser Ser Glu Thr Ile Val Gly Val Ser Ala Gly Ile Ile Val Val
 65 70 75 80
 Gly Thr Met Leu Gly Ala Phe Ala Ala Pro Val Leu Ala Ala Gly Ile
 85 90 95
 Ile Ser Phe Gly Thr Leu Leu Pro Ile Phe Trp Gln Gly Ser Asp Pro
 100 105 110
 Ala Asn Val Trp Gln Asp Leu Leu Asn Ile Gly Gly Arg Pro Ile Gln
 115 120 125
 Glu Ile Asp Lys Asn Ile Ile Asn Val Leu Thr Ser Ile Val Thr Pro
 130 135 140
 Ile Lys Asn Gln Leu Asp Lys Tyr Gln Glu Phe Phe Asp Lys Trp Glu
 145 150 155 160
 Pro Ala Arg Thr His Ala Asn Ala Lys Ala Val His Asp Leu Phe Thr
 165 170 175
 Thr Leu Glu Pro Ile Ile Asp Lys Asp Leu Asp Met Leu Lys Asn Asn
 180 185 190
 Ala Ser Tyr Arg Ile Pro Thr Leu Pro Ala Tyr Ala Gln Ile Ala Thr
 195 200 205
 Trp His Leu Asn Leu Leu Lys His Ala Ala Thr Tyr Tyr Asn Ile Trp
 210 215 220
 Leu Gln Asn Gln Gly Ile Asn Pro Ser Thr Phe Asn Ser Ser Asn Tyr
 225 230 235 240
 Tyr Gln Gly Tyr Leu Lys Arg Lys Ile Gln Glu Tyr Thr Asp Tyr Cys
 245 250 255
 Ile Gln Thr Tyr Asn Ala Gly Leu Thr Met Ile Arg Thr Asn Thr Asn
 260 265 270
 Ala Thr Trp Asn Met Tyr Asn Thr Tyr Arg Leu Glu Met Thr Leu Thr
 275 280 285
 Val Leu Asp Leu Ile Ala Ile Phe Pro Asn Tyr Asp Pro Glu Lys Tyr
 290 295 300
 Pro Ile Gly Val Lys Ser Glu Leu Ile Arg Glu Val Tyr Thr Asn Val

305 310 315 320
 Asn Ser Asp Thr Phe Arg Thr Ile Thr Glu Leu Glu Asn Gly Leu Thr
 325 330 335
 Arg Asn Pro Thr Leu Phe Thr Trp Ile Asn Gln Gly Arg Phe Tyr Thr
 340 345 350
 Arg Asn Ser Arg Asp Ile Leu Asp Pro Tyr Asp Ile Phe Ser Phe Thr
 355 360 365
 Gly Asn Gln Met Ala Phe Thr His Thr Asn Asp Asp Arg Asn Ile Ile
 370 375 380
 Trp Gly Ala Val His Gly Asn Ile Ile Ser Gln Asp Thr Ser Lys Val
 385 390 395 400
 Phe Pro Phe Tyr Arg Asn Lys Pro Ile Asp Lys Val Glu Ile Val Arg
 405 410 415
 His Arg Glu Tyr Ser Asp Ile Ile Tyr Glu Met Ile Phe Phe Ser Asn
 420 425 430
 Ser Ser Glu Val Phe Arg Tyr Ser Ser Asn Ser Thr Ile Glu Asn Asn
 435 440 445
 Tyr Lys Arg Thr Asp Ser Tyr Met Ile Pro Lys Gln Thr Trp Lys Asn
 450 455 460
 Glu Glu Tyr Gly His Thr Leu Ser Tyr Ile Lys Thr Asp Asn Tyr Ile
 465 470 475 480
 Phe Ser Val Val Arg Glu Arg Arg Arg Val Ala Phe Ser Trp Thr His
 485 490 495
 Thr Ser Val Asp Phe Gln Asn Thr Ile Asp Leu Asp Asn Ile Thr Gln
 500 505 510
 Ile His Ala Leu Lys Ala Leu Lys Val Ser Ser Asp Ser Lys Ile Val
 515 520 525
 Lys Gly Pro Gly His Thr Gly Gly Asp Leu Val Ile Leu Lys Asp Ser
 530 535 540
 Met Asp Phe Arg Val Arg Phe Leu Lys Asn Val Ser Arg Gln Tyr Gln
 545 550 555 560
 Val Arg Ile Arg Tyr Ala Thr Asn Ala Pro Lys Thr Thr Val Phe Leu
 565 570 575
 Thr Gly Ile Asp Thr Ile Ser Val Glu Leu Pro Ser Thr Thr Ser Arg
 580 585 590
 Gln Asn Pro Asn Ala Thr Asp Leu Thr Tyr Ala Asp Phe Gly Tyr Val
 595 600 605
 Thr Phe Pro Arg Thr Val Pro Asn Lys Thr Phe Glu Gly Glu Asp Thr
 610 615 620
 Leu Leu Met Thr Leu Tyr Gly Thr Pro Asn His Ser Tyr Asn Ile Tyr
 625 630 635 640
 Ile Asp Lys Ile Glu Phe Ile Pro Ile Thr Gln Ser Val Leu Asp Tyr
 645 650 655
 Thr Glu Lys Gln Asn Ile Glu Lys Thr Gln Lys Ile Val Asn Asp Leu
 660 665 670
 Phe Val Asn
 675

<210> 44
 <211> 648
 <212> PRT
 <213> Bacillus thuringiensis

<400> 44
 Met His Tyr Tyr Gly Asn Arg Asn Glu Tyr Asp Ile Leu Asn Ala Ser
 1 5 10 15
 Ser Asn Asp Ser Asn Met Ser Asn Thr Tyr Pro Arg Tyr Pro Leu Ala
 20 25 30
 Asn Pro Gln Asp Leu Met Gln Asn Thr Asn Tyr Lys Asp Trp Leu
 35 40 45
 Asn Val Cys Glu Gly Tyr His Ile Glu Asn Pro Arg Glu Ala Ser Val
 50 55 60
 Arg Ala Gly Leu Gly Lys Gly Leu Gly Ile Val Ser Thr Ile Val Gly
 65 70 75 80
 Phe Phe Gly Gly Ser Ile Ile Leu Asp Thr Ile Gly Leu Phe Tyr Gln
 85 90 95
 Ile Ser Glu Leu Leu Trp Pro Glu Asp Asp Thr Gln Gln Tyr Thr Trp

- 82 -

645

<210> 45
 <211> 682
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 45
 Met Asn Ser Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Leu Asp Ala Lys
 1 5 10 15
 Arg Asn Thr Cys His Met Ser Asn Cys Tyr Pro Lys Tyr Pro Leu Ala
 20 25 30
 Asn Asp Pro Gln Met Tyr Leu Arg Asn Thr His Tyr Lys Asp Trp Ile
 35 40 45
 Asn Met Cys Glu Glu Ala Ser Tyr Ala Ser Ser Gly Pro Ser Gln Leu
 50 55 60
 Phe Lys Val Gly Gly Ser Ile Val Ala Lys Ile Leu Gly Met Ile Pro
 65 70 75 80
 Glu Val Gly Pro Leu Leu Ser Trp Met Val Ser Leu Phe Trp Pro Thr
 85 90 95
 Ile Glu Glu Lys Asn Thr Val Trp Glu Asp Met Ile Lys Tyr Val Ala
 100 105 110
 Asn Leu Leu Lys Gln Glu Leu Thr Asn Asp Thr Leu Asn Arg Ala Thr
 115 120 125
 Ser Asn Leu Ser Gly Leu Asn Glu Ser Leu Asn Ile Tyr Asn Arg Ala
 130 135 140
 Leu Ala Ala Trp Lys Gln Asn Lys Asn Asn Phe Ala Ser Gly Glu Leu
 145 150 155 160
 Ile Arg Ser Tyr Ile Asn Asp Leu His Ile Leu Phe Thr Arg Asp Ile
 165 170 175
 Gln Ser Asp Phe Ser Leu Gly Gly Tyr Glu Thr Val Leu Leu Pro Ser
 180 185 190
 Tyr Ala Ser Ala Ala Asn Leu His Leu Leu Leu Leu Arg Asp Val Ala
 195 200 205
 Ile Tyr Gly Lys Glu Leu Gly Tyr Pro Ser Thr Asp Val Glu Phe Tyr
 210 215 220
 Tyr Asn Glu Gln Lys Tyr Tyr Thr Glu Lys Tyr Ser Asn Tyr Cys Val
 225 230 235 240
 Asn Thr Tyr Lys Ser Gly Leu Glu Ser Lys Lys Gln Ile Gly Trp Ser
 245 250 255
 Asp Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu Ser Val Leu Asp Ile
 260 265 270
 Val Ala Leu Phe Pro Leu Tyr Asp Thr Gly Leu Tyr Pro Ser Lys Asp
 275 280 285
 Gly Lys Ile His Val Lys Ala Glu Leu Thr Arg Glu Ile Tyr Ser Asp
 290 295 300
 Val Ile Asn Asp His Val Tyr Gly Leu Met Val Pro Tyr Ile Ser Phe
 305 310 315 320
 Glu His Ala Glu Ser Leu Tyr Thr Arg Arg Pro His Ala Phe Thr Trp
 325 330 335
 Leu Lys Gly Phe Arg Phe Val Thr Asn Ser Ile Asn Ser Trp Thr Phe
 340 345 350
 Leu Ser Gly Gly Glu Asn Arg Tyr Phe Leu Thr His Gly Glu Gly Thr
 355 360 365
 Ile Tyr Asn Gly Pro Phe Leu Gly Gln Asp Thr Glu Tyr Gly Gly Thr
 370 375 380
 Ser Ser Tyr Ile Asp Ile Ser Asn Asn Ser Ser Ile Tyr Asn Leu Trp
 385 390 395 400
 Thr Lys Asn Tyr Glu Trp Ile Tyr Pro Trp Thr Asp Pro Val Asn Ile
 405 410 415
 Thr Lys Ile Asn Phe Ser Ile Thr Asp Asn Ser Asn Ser Ser Glu Ser
 420 425 430
 Ile Tyr Gly Ala Glu Arg Met Asn Lys Pro Thr Val Arg Thr Asp Phe
 435 440 445
 Asn Phe Leu Leu Asn Arg Ala Gly Asn Gly Pro Thr Thr Tyr Asn Asp
 450 455 460
 Tyr Asn His Ile Leu Ser Tyr Met Leu Ile Asn Gly Glu Thr Phe Gly

465 470 475 480
 Gln Lys Arg His Gly Tyr Ser Phe Ala Phe Thr His Ser Ser Val Asp
 485 490 495
 Arg Tyr Asn Thr Ile Val Pro Asp Lys Ile Val Gln Ile Pro Ala Val
 500 505 510
 Lys Thr Asn Leu Val Gly Ala Asn Ile Ile Lys Gly Pro Gly His Thr
 515 520 525
 Gly Gly Asp Leu Leu Lys Leu Glu Tyr Glu Arg Phe Leu Ser Leu Arg
 530 535 540
 Ile Lys Leu Ile Ala Ser Met Thr Phe Arg Ile Arg Ile Arg Tyr Ala
 545 550 555 560
 Ser Asn Ile Ser Gly Gln Met Met Ile Asn Ile Gly Tyr Gln Asn Pro
 565 570 575
 Thr Tyr Phe Asn Ile Ile Pro Thr Thr Ser Arg Asp Tyr Thr Glu Leu
 580 585 590
 Lys Phe Glu Asp Phe Gln Leu Val Asp Thr Ser Tyr Ile Tyr Ser Gly
 595 600 605
 Gly Pro Ser Ile Ser Ser Asn Thr Leu Trp Leu Asp Asn Phe Ser Asn
 610 615 620
 Gly Pro Val Ile Ile Asp Lys Ile Glu Phe Ile Pro Leu Gly Ile Thr
 625 630 635 640
 Leu Asn Gln Ala Gln Gly Tyr Asp Thr Tyr Asp Gln Asn Ala Asn Gly
 645 650 655
 Met Tyr His Gln Asn Tyr Ser Asn Ser Gly Tyr Asn Tyr Asn Gln Glu
 660 665 670
 Tyr Asn Thr Tyr Tyr Gln Ser Tyr Asn Asn
 675 680

<210> 46

<211> 529

<212> PRT

<213> *Bacillus thuringiensis*

<400> 46

Val Asn Phe Met Leu Thr Ser Gly Ala Lys Asn Met Leu Lys Leu Glu
 1 5 10 15
 Thr Thr Asp Tyr Glu Ile Asp Gln Met Ala Asn Ala Ile Glu Asn Met
 20 25 30
 Ser Gly Glu Gln Tyr Ser Gln Glu Lys Met Met Gln Trp His Asp Ile
 35 40 45
 Lys Tyr Ala Lys Gln Leu Ser Gln Ala Arg Asn Leu Leu Gln Asn Gly
 50 55 60
 Asp Phe Glu Asp Leu Phe Ser Gly Trp Thr Thr Ser Asn Gln Met Ser
 65 70 75 80
 Ile Gln Ala Asp Asn Ala Thr Phe Lys Gly Asn Tyr Leu His Met Ser
 85 90 95
 Gly Ala Arg Asp Ile Tyr Gly Thr Ile Phe Pro Thr Tyr Ile Tyr Gln
 100 105 110
 Lys Ile Asp Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Leu Val Arg
 115 120 125
 Gly Phe Val Gly Ser Ser Lys Asp Leu Glu Leu Met Val Met Arg Tyr
 130 135 140
 Gly Lys Glu Ile Asp Thr Val Met Asn Val Pro Asn Asp Ile Pro Tyr
 145 150 155 160
 Val Pro Ser Met Pro Val Cys Asn Glu Leu Tyr Asp Gly Gln Gln Pro
 165 170 175
 Tyr Pro Asn Arg His Val Gly Tyr Tyr Asn Pro Met Pro Val Ser Gln
 180 185 190
 Pro Ser Tyr Thr Ser Asp Thr Cys Gln Cys Thr Pro Gly Lys Lys His
 195 200 205
 Val Val Cys His Asp Ser His Gln Phe Lys Phe His Ile Asp Thr Gly
 210 215 220
 Glu Val Asp Tyr Asn Thr Asn Leu Gly Ile Trp Val Leu Phe Lys Ile
 225 230 235 240
 Ser Ser Pro Asp Gly Tyr Ala Thr Leu Asp Asn Leu Glu Val Ile Glu
 245 250 255
 Glu Gly Pro Val Arg Gly Glu Ala Val Thr His Val Lys Gln Lys Glu

260 265 270
 Lys Lys Trp Asn Gln Gln Met Glu Lys Lys Arg Met Glu Thr Lys Arg
 275 280 285
 Val Tyr Asp Arg Ala Lys Gln Ala Val Asp Ala Leu Phe Thr Gly Glu
 290 295 300
 Glu Leu Asn Tyr Asp Val Thr Leu Ser His Ile Lys Asn Ala Asp Asp
 305 310 315 320
 Leu Val Gln Ser Ile Pro Tyr Val His Asn Glu Trp Leu Pro Asp Phe
 325 330 335
 Pro Gly Met Asn Tyr Asp Ile Tyr Gln Glu Leu Asn Ala Arg Ile Met
 340 345 350
 Gln Ala Arg Tyr Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp
 355 360 365
 Phe Ala Gln Gly Leu Gln Gly Trp His Ala Glu Gly Lys Val Glu Val
 370 375 380
 Gln Gln Met Asn Gly Thr Ser Val Leu Val Leu Ser Asn Trp Ser Ser
 385 390 395 400
 Gly Val Ser Gln Asn Leu His Val Gln His Pro His Gly Tyr Leu Leu
 405 410 415
 Arg Val Ser Ala Lys Lys Glu Gly Ser Gly Lys Gly Tyr Val Thr Arg
 420 425 430
 Met Ser Cys Asn Gly Lys Gln Glu Thr Leu Thr Phe Thr Ser Cys Asp
 435 440 445
 Gly Gly Tyr Met Thr Lys Thr Val Glu Val Phe Pro Glu Ser Asp Arg
 450 455 460
 Val Arg Ile Glu Ile Gly Glu Thr Glu Gly Ser Phe Tyr Ile Glu Ser
 465 470 475 480
 Ile Glu Leu Ile Cys Met Asn Gly Tyr Thr Ser Asn Asn Asn Gln Asn
 485 490 495
 Met Ser Asn Met Tyr Asp Gln Ser Tyr Ser Gly Asn Tyr Ser Gln Asn
 500 505 510
 Thr Ser Asp Met Tyr Asp Gln Gly Ser Val Ala Lys Phe Glu Lys
 515 520 525
 Glu

<210> 47

<211> 674

<212> PRT

<213> *Bacillus thuringiensis*

<400> 47

Met Asn Gln Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Leu Glu Ser Ser
 1 5 10 15
 Gln Asn Asn Met Asn Met Pro Asn Arg Tyr Pro Phe Ala Asp Asp Pro
 20 25 30
 Asn Ala Val Met Lys Asn Gly Asn Tyr Lys Asp Trp Val Asn Glu Cys
 35 40 45
 Glu Gly Ser Asn Ile Ser Pro Ser Pro Ala Ala Ala Ile Thr Ser Lys
 50 55 60
 Ile Val Ser Ile Val Leu Lys Thr Leu Ala Lys Ala Val Ala Ser Ser
 65 70 75 80
 Leu Ala Asp Ser Ile Lys Ser Ser Leu Gly Ile Ser Lys Thr Ile Thr
 85 90 95
 Glu Asn Asn Val Ser Gln Val Ser Met Val Gln Val His Gln Ile Ile
 100 105 110
 Asn Arg Arg Ile Gln Glu Thr Ile Leu Asp Leu Gly Glu Ser Ser Leu
 115 120 125
 Asn Gly Leu Val Ala Ile Tyr Asn Arg Asp Tyr Leu Gly Ala Leu Glu
 130 135 140
 Ala Trp Asn Asn Asn Lys Ser Asn Ile Asn Tyr Gln Thr Asn Val Ala
 145 150 155 160
 Glu Ala Phe Lys Thr Val Glu Arg Glu Phe Thr Lys Leu Lys Gly
 165 170 175
 Ile Tyr Arg Thr Ser Ser Ser Gln Ile Thr Leu Leu Pro Thr Phe Thr
 180 185 190
 Gln Ala Ala Asn Leu His Leu Ser Met Leu Arg Asp Ala Val Met Tyr

195					200					205					
Gln	Glu	Gly	Trp	Asn	Leu	Gln	Ser	His	Ile	Asn	Tyr	Ser	Lys	Glu	Leu
210					215					220					
Asp	Asp	Ala	Leu	Glu	Asp	Tyr	Thr	Asn	Tyr	Cys	Val	Glu	Val	Tyr	Thr
225					230					235					
Lys	Gly	Leu	Asn	Ala	Leu	Arg	Gly	Ser	Thr	Ala	Ile	Asp	Trp	Leu	Glu
245					250					255					
Phe	Asn	Ser	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val
260					265					270					
Ala	Ile	Phe	Pro	Asn	Tyr	Asn	Pro	Val	Arg	Tyr	Pro	Leu	Ser	Thr	Lys
275					280					285					
Ile	Ser	Leu	Ser	Arg	Lys	Ile	Tyr	Thr	Asp	Pro	Val	Gly	Arg	Thr	Asp
290					295					300					
Ser	Pro	Ser	Phe	Gly	Asp	Trp	Thr	Asn	Thr	Gly	Arg	Thr	Leu	Ala	Asn
305					310					315					
Phe	Asn	Asp	Leu	Glu	Arg	Glu	Val	Thr	Asp	Ser	Pro	Ser	Leu	Val	Lys
325					330					335					
Trp	Leu	Gly	Asp	Met	Thr	Ile	Tyr	Thr	Gly	Ala	Ile	Asp	Ser	Tyr	Arg
340					345					350					
Pro	Thr	Ser	Pro	Gly	Asp	Arg	Ile	Gly	Val	Trp	Tyr	Gly	Asn	Ile	Asn
355					360					365					
Ala	Phe	Tyr	His	Thr	Gly	Arg	Thr	Asp	Val	Val	Met	Phe	Arg	Gln	Thr
370					375					380					
Gly	Asp	Thr	Ala	Tyr	Glu	Asp	Pro	Ser	Thr	Phe	Ile	Ser	Asn	Ile	Leu
385					390					395					
Tyr	Asp	Asp	Ile	Tyr	Lys	Leu	Asp	Leu	Arg	Ala	Ala	Ala	Val	Ser	Thr
405					410					415					
Ile	Gln	Gly	Ala	Met	Asp	Thr	Thr	Phe	Gly	Val	Ser	Ser	Ser	Arg	Phe
420					425					430					
Phe	Asp	Ile	Arg	Gly	Arg	Asn	Gln	Leu	Tyr	Gln	Ser	Asn	Lys	Pro	Tyr
435					440					445					
Pro	Ser	Leu	Pro	Ile	Thr	Ile	Thr	Phe	Pro	Gly	Glu	Glu	Ser	Ser	Glu
450					455					460					
Gly	Asn	Ala	Asn	Asp	Tyr	Ser	His	Leu	Leu	Cys	Asp	Val	Lys	Ile	Leu
465					470					475					
Gln	Glu	Asp	Ser	Ser	Asn	Ile	Cys	Glu	Gly	Arg	Ser	Ser	Leu	Leu	Ser
485					490					495					
His	Ala	Trp	Thr	His	Ala	Ser	Leu	Asp	Arg	Asn	Asn	Thr	Ile	Leu	Pro
500					505					510					
Asp	Glu	Ile	Thr	Gln	Ile	Pro	Ala	Val	Thr	Ala	Tyr	Glu	Leu	Arg	Gly
515					520					525					
Asn	Ser	Ser	Val	Val	Ala	Gly	Pro	Gly	Ser	Thr	Gly	Gly	Asp	Leu	Val
530					535					540					
Lys	Met	Ser	Tyr	His	Ser	Val	Trp	Ser	Phe	Lys	Val	Tyr	Cys	Ser	Glu
545					550					555					
Leu	Lys	Asn	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	His	Gly	Asn	Cys
565					570					575					
Gln	Phe	Leu	Met	Lys	Arg	Trp	Pro	Ser	Thr	Gly	Val	Ala	Pro	Arg	Gln
580					585					590					
Trp	Ala	Arg	His	Asn	Val	Gln	Gly	Thr	Phe	Ser	Asn	Ser	Met	Arg	Tyr
595					600					605					
Glu	Ala	Phe	Lys	Tyr	Leu	Asp	Ile	Phe	Thr	Ile	Thr	Pro	Glu	Glu	Asn
610					615					620					
Asn	Phe	Ala	Phe	Thr	Ile	Asp	Leu	Glu	Ser	Gly	Gly	Asp	Leu	Phe	Ile
625					630					635					
Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Ser	Gly	Ser	Ala	Phe	Glu	Tyr	Glu
645					650					655					
Gly	Lys	Gln	Asn	Ile	Glu	Lys	Thr	Gln	Lys	Ala	Val	Asn	Asp	Leu	Phe
660					665					670					
Ile Asn															

<210> 48

<211> 675

<212> PRT

<213> Bacillus thuringiensis

<400> 48

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Met Asn Pro Tyr Gln Asn Lys Ser Glu Cys Glu Ile Leu Asn Ala Pro
 1          5          10          15
Leu Asn Asn Ile Asn Met Pro Asn Arg Tyr Pro Phe Ala Asn Asp Pro
 20          25          30
Asn Ala Val Met Lys Asn Gly Asn Tyr Lys Asp Trp Leu Asn Glu Cys
 35          40          45
Asp Gly Ile Thr Pro Ser Ile Phe Gly Thr Leu Gly Val Leu Ala Ser
 50          55          60
Ile Val Ile Ser Thr Ile Asn Leu Ala Thr Ser Pro Ser Ile Gly Asp
 65          70          75          80
Ala Phe Ala Leu Val Ser Ser Ile Gly Glu Tyr Trp Pro Glu Thr Lys
 85          90          95
Thr Ser Phe Pro Leu Ser Val Ala Asp Val Asn Arg Leu Ile Arg Glu
100          105          110
Ala Leu Asp Gln Asn Ala Ile Asn Arg Ala Thr Gly Lys Phe Asn Gly
115          120          125
Leu Met Asp Thr Tyr Asn Thr Val Tyr Leu Lys Asn Leu Gln Asp Trp
130          135          140
Tyr Asp Thr Arg Ile Pro Ala Asn Pro Gln Gly Asp Ser Gln Leu Arg
145          150          155          160
Glu Ala Ala Arg Arg Ser Leu Glu Glu Ile Glu Arg Asp Phe Arg Lys
165          170          175
Ala Leu Ala Gly Glu Phe Ala Glu Ala Gly Ser Gln Ile Val Leu Leu
180          185          190
Pro Ile Tyr Ala Gln Ala Ala Asn Ile His Leu Leu Ile Leu Lys Asp
195          200          205
Ala Met Gln Phe Arg Thr Asp Leu Gly Leu Ile Arg Pro Val Gly Val
210          215          220
Pro Ile Thr Thr Ser Ala Glu Asp Pro Phe Glu Ser Glu Phe Leu Leu
225          230          235          240
Arg Ile Lys Lys Tyr Thr Asp His Cys Ile Ser Tyr Tyr Asp Asp Gly
245          250          255
Leu Ala Lys Ile Arg Ser Arg Gly Ser Asp Gly Glu Thr Trp Trp Glu
260          265          270
Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu Val
275          280          285
Ala Leu Tyr Pro Thr His Asn Ile Lys Leu Tyr Pro Ile Pro Thr Gln
290          295          300
Thr Glu Leu Ser Arg Val Val Tyr Thr Asp Pro Val Gly Cys Phe Gly
305          310          315          320
Asn Arg Lys Ser Asp Ile Phe Ser Arg Leu Asn Phe Asp Tyr Leu Glu
325          330          335
Asn Arg Leu Thr Arg Pro Arg Glu Pro Phe Asn Tyr Leu Asn Ser Val
340          345          350
Gln Leu Phe Ala Ser Thr Val Ser Asn Ser Asn Asn Gly Glu Val Leu
355          360          365
Arg Gly Asn Leu Asn Lys Ile Met Phe Glu Gly Gly Trp Thr Ala Ser
370          375          380
Arg Ser Gly Asp Gly Val Thr Thr Gly Thr Pro Phe Ser Thr Met Asp
385          390          395          400
Trp Ser Tyr Gly Trp Gly Tyr Pro Arg Lys His Tyr Ala Glu Ile Thr
405          410          415
Ser Arg Ser Gln Ala Leu Pro Gly Leu Asn Asn Ser Ile His Val Ile
420          425          430
Val Gly Ile Asp Ser Phe Arg Ala Ile Gly Pro Gly Gly Gln Gly Asp
435          440          445
His Thr Phe Ser Leu Pro Gly Gly Asp Met Tyr Asp Cys Gly Lys Val
450          455          460
Gln Ile Asn Pro Leu Glu Asp Tyr Arg Asn Ser Asp His Trp Ile Ser
465          470          475          480
Asp Met Met Thr Ile Asn Gln Ser Val Gln Leu Ala Ser Asn Pro Thr
485          490          495
Gln Thr Phe Ala Phe Ser Ala Leu Ser Leu Gly Trp His His Ser Ser
500          505          510
Ala Gly Asn Arg Asn Val Tyr Val Tyr Asp Lys Ile Thr Gln Ile Pro
515          520          525
Ala Thr Lys Thr Val Arg Glu His Pro Met Ile Lys Gly Pro Gly Phe

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530 535 540
 Thr Gly Gly Asp Leu Ala Asp Leu Ser Ser Asn Ser Asp Ile Leu Gln
 545 550 555 560
 Tyr Asp Leu Arg Ser Asp Tyr Asp Asp Arg Leu Thr Glu Asp Val Pro
 565 570 575
 Phe Arg Ile Arg Ile Arg Cys Ala Ser Ile Gly Val Ser Thr Ile Ser
 580 585 590
 Val Asp Asn Trp Gly Ser Ser Ser Pro Gln Val Thr Val Ala Ser Thr
 595 600 605
 Ala Ala Ser Leu Asp Thr Leu Lys Tyr Glu Ser Phe Gln Tyr Val Ser
 610 615 620
 Ile Pro Gly Asn Tyr Tyr Phe Asp Ser Ala Pro Arg Ile Arg Leu Leu
 625 630 635 640
 Arg Gln Pro Gly Arg Leu Leu Val Asp Arg Ile Glu Ile Ile Pro Val
 645 650 655
 Asn Phe Phe Pro Leu Ser Glu Gln Glu Asn Lys Ser Val Asp Ser Leu
 660 665 670
 Phe Ile Asn
 675

<210> 49
 <211> 659
 <212> PRT
 <213> Bacillus thuringiensis

<400> 49
 Asn Ser Tyr Glu Asn Lys Asn Glu Tyr Glu Ile Leu Asn Asp Ser Lys
 1 5 10 15
 Lys Ser Asn Met Ser Asn Pro Tyr Leu Arg Tyr Pro Leu Ala Asn Asp
 20 25 30
 Ser Leu Ala Ser Met Gln Asn Thr Asn Tyr Lys Asp Trp Leu Thr Met
 35 40 45
 Cys Asp Arg Thr Asp Thr Asp Val Leu Ser Ser Arg Gly Ala Val Ser
 50 55 60
 Thr Gly Val Gly Met Leu Ser Thr Ile Leu Ser Leu Phe Gly Ile Pro
 65 70 75 80
 Leu Ile Gly Glu Gly Ile Asp Leu Leu Leu Gly Ala Ala Asp Phe Leu
 85 90 95
 Trp Pro Glu Ser Asp Gly Gly His Gln Tyr Thr Trp Glu Asp Leu Met
 100 105 110
 Asn His Ile Glu Glu Leu Met Asp Glu Arg Leu Glu Thr Glu Lys Arg
 115 120 125
 Thr Thr Ala Leu Asp Asp Leu Arg Gly Leu Lys Ala Leu Leu Gly Leu
 130 135 140
 Phe Arg Asp Ala Phe Asp Ser Trp Glu Lys Asn Gln Asn Asp Pro Ile
 145 150 155 160
 Ala Lys Asn Arg Val Gly Gly Tyr Phe Glu Asp Val His Thr His Phe
 165 170 175
 Val Lys Asp Met Ala Ser Ile Phe Ser Ala Thr Asn Tyr Glu Val Leu
 180 185 190
 Leu Leu Pro Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu Leu
 195 200 205
 Arg Glu Gly Val Ile Tyr Gly Ser Arg Trp Gly Ile Ala Pro Ala Ala
 210 215 220
 Asp Phe Tyr His Asp Gln Leu Leu Lys Tyr Thr Ala Ile Tyr Ala Asn
 225 230 235 240
 His Cys Val Thr Trp Tyr Asn Asn Gly Leu Ala Gln Gln Lys Glu Leu
 245 250 255
 Phe Ala Lys Ser Pro Asn Trp Asn Arg Phe Asn Ala Tyr Arg Arg Asp
 260 265 270
 Met Thr Ile Thr Val Leu Asp Ile Ile Ala Leu Phe Pro Thr Tyr Asp
 275 280 285
 Ala Arg Leu Tyr Thr Lys Pro Ile Lys Thr Glu Leu Thr Arg Glu Ile
 290 295 300
 Tyr Ser Asp Val Leu Asn Leu Asp Val Tyr Gly Val Gln Gln Thr Asp
 305 310 315 320
 Leu Asn Lys Asn Glu Ala Ala Phe Thr Arg Ser Pro His Leu Val Thr

325 330 335
 Arg Leu Arg Gly Phe Asp Phe Tyr Thr Arg Thr Lys Tyr Ala Tyr Trp
 340 345 350
 Arg Tyr Leu Ala Gly His Thr Asn Tyr Phe Ser Phe Thr Gly Asn Gly
 355 360 365
 Thr Ile Tyr Ser Ser Ser Phe Asn Asn Trp Tyr Asp Thr Asp Met Thr
 370 375 380
 Lys Ser Thr Ile Asn Ile Pro Asp Tyr Ala Asn Ile Tyr Lys Leu Trp
 385 390 395 400
 Thr Lys Ser Tyr Thr Asn Ile Ser Pro Tyr Thr Asp Pro Val Gly Ile
 405 410 415
 Ser Gln Met Gln Phe Ser Leu Thr Asn Asn Gln Gln Leu Thr Tyr Thr
 420 425 430
 Gly Thr Ser Ala Pro Lys Tyr Pro Val Arg Glu Thr Phe Phe Glu Ile
 435 440 445
 Pro Pro Thr Asp Glu Lys Pro Leu Thr Tyr Glu Asn Tyr Ser His Ile
 450 455 460
 Leu Ser Tyr Met Thr Ser Ala Gln His Phe Gly Asp Lys Lys Ile Gly
 465 470 475 480
 Tyr Thr Phe Ala Trp Met His Glu Ser Val Asp Phe Asp Asn Arg Val
 485 490 495
 Asp Pro Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Gly Asp Tyr Leu
 500 505 510
 Gln Tyr Gly Tyr Val Lys Gln Gly Pro Gly His Thr Gly Gly Asp Leu
 515 520 525
 Val Ser Met Ile Arg Thr Asp Arg Leu Gly Ile Asn Val Tyr Phe Pro
 530 535 540
 Gln Pro Leu Asp Tyr Arg Ile Arg Ile Arg Tyr Ser Thr Ser Ser Asn
 545 550 555 560
 Gly Tyr Leu Tyr Ile Tyr Ser Pro Asn Thr Lys Ile Val Tyr Leu Pro
 565 570 575
 Pro Thr Thr Leu Val Asp Gly Gln Pro Thr Phe Asp Pro Met Asp Phe
 580 585 590
 Ser Ala Phe Arg Val Val Glu Val Pro Ala Ser Phe Arg Ala Ser Val
 595 600 605
 Ala Gly Tyr Thr Asn Phe Thr Ile Glu Ala Gly Phe Gly Pro Val Tyr
 610 615 620
 Ile Asp Lys Ile Glu Phe Ile Pro Asp Asn Thr Thr Thr Leu Glu Tyr
 625 630 635 640
 Glu Gly Gly Arg Asp Leu Glu Lys Thr Lys Asn Ala Val Asn Asp Leu
 645 650 655
 Phe Thr Asn

<210> 50

<211> 558

<212> PRT

<213> Bacillus thuringiensis

<400> 50

Met Phe Ile Ser Asn Ile Lys Asn Thr Leu Lys Ile Glu Thr Thr Asp
 1 5 10 15
 Tyr Glu Ile Asp Gln Ala Ala Ile Ser Ile Glu Cys Met Ser Asn Glu
 20 25 30
 His Ser Ser Lys Glu Glu Met Met Leu Trp Asp Glu Val Lys Gln Ala
 35 40 45
 Lys Gln Leu Ser Trp Ser Arg Asn Leu Leu Tyr Asn Gly Asp Phe Glu
 50 55 60
 Asp Val Ser Asn Gly Trp Lys Thr Ser Asn Thr Ile Glu Ile Arg Glu
 65 70 75 80
 Asn Ser Pro Val Phe Lys Gly His Tyr Leu His Met Phe Gly Ala Arg
 85 90 95
 Asp Ile Asp Gly Thr Leu Phe Pro Thr Tyr Ile Tyr Gln Lys Ile Glu
 100 105 110
 Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Arg Val Arg Gly Phe Val
 115 120 125
 Gly Ser Ser Lys Asp Leu Lys Leu Met Val Thr Arg Tyr Gly Lys Glu

130 135 140
 Ile Asp Ala Met Met Asn Val Pro Asn Asp Leu Ala Tyr Met Gln Pro
 145 150 155 160
 Thr Pro Ser Cys Gly Asp Ser Arg Cys Glu Ser Ser Ser Arg Tyr Val
 165 170 175
 Ser Gln Gly Tyr Pro Thr Pro Val Thr Asp Gly Tyr Ala Ser Gly Arg
 180 185 190
 Tyr Ala Cys Gln Ser Asn Arg Gly Thr Lys His Val Lys Cys His Asp
 195 200 205
 Arg His Pro Phe Asp Phe His Ile Asp Thr Gly Glu Leu Asp Thr Asn
 210 215 220
 Thr Asn Val Gly Ile Asp Val Leu Phe Lys Ile Ser Asn Pro Asp Gly
 225 230 235 240
 Tyr Ala Thr Leu Gly Asn Leu Glu Val Ile Glu Glu Gly Pro Leu Thr
 245 250 255
 Gly Glu Ala Leu Thr His Val Lys Gln Lys Glu Lys Lys Trp Lys Gln
 260 265 270
 His Met Glu Lys Lys Arg Trp Glu Thr Gln Gln Ala Tyr Asp Pro Ala
 275 280 285
 Lys Gln Ala Val Asp Ala Leu Phe Thr Asn Glu Gln Glu Leu His Tyr
 290 295 300
 His Ile Thr Leu Asp His Ile Gln Asn Ala Asp Arg Leu Ile Gln Ala
 305 310 315 320
 Ile Pro Tyr Val Tyr His Ala Trp Leu Pro Asp Ala Pro Gly Met Asn
 325 330 335
 Tyr Asp Gly Tyr Gln Gly Leu Asn Ala Arg Ile Met Gln Ala Tyr Asn
 340 345 350
 Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp Phe Thr Gln Gly
 355 360 365
 Leu Thr Gly Trp His Ala Ala Gly Lys Ala Met Val Gln Gln Met Asp
 370 375 380
 Gly Ala Ser Val Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln
 385 390 395 400
 Asn Leu His Val Gln Glu His His Gly Tyr Met Leu Arg Val Ile Ala
 405 410 415
 Lys Lys Glu Gly Pro Gly Lys Gly Tyr Val Thr Met Met Asp Cys Asn
 420 425 430
 Gly Asn Arg Glu Thr Leu Lys Phe Thr Ser Cys Glu Glu Gly Tyr Met
 435 440 445
 Thr Lys Thr Val Glu Val Phe Pro Glu Ser Asp Arg Val Arg Ile Glu
 450 455 460
 Ile Gly Glu Thr Glu Gly Thr Phe Tyr Val Asp Ser Ile Glu Leu Leu
 465 470 475 480
 Cys Met Gln Gly Tyr Ala Ser Asn Asn Asn Pro His Thr Gly Asn Met
 485 490 495
 Tyr Gly Gln Ser Tyr Asn Gly Asn Tyr Asn Gln Asn Thr Ser Asp Val
 500 505 510
 Tyr His Gln Gly Tyr Thr Asn Asn Tyr Asn Gln Asn Ser Ser Asn Met
 515 520 525
 Tyr Asn Gln Asn Tyr Thr His Asn Asp Asp Leu His Ser Gly Cys Thr
 530 535 540
 Cys Asn Gln Gly His Asn Ser Gly Cys Thr Cys Ser Gln Gly
 545 550 555

<210> 51

<211> 666

<212> PRT

<213> *Bacillus thuringiensis*

<400> 51

Asn Ser Tyr Glu Asn Lys Asn Glu Tyr Glu Ile Leu Glu Ser Ser Ser
 1 5 10 15
 Asn Asn Thr Asn Met Pro Asn Arg Tyr Pro Phe Ala Asn Asp Arg Asp
 20 25 30
 Met Ser Thr Met Ser Phe Asn Asp Cys Gln Gly Ile Ser Trp Asp Glu
 35 40 45
 Ile Trp Glu Ser Ala Glu Thr Ile Thr Ser Ile Gly Ile Asp Leu Ile

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50          55          60
Glu Phe Leu Met Glu Pro Ser Leu Gly Gly Ile Asn Thr Leu Phe Ser
65          70          75          80
Ile Ile Gly Lys Leu Ile Pro Thr Asn His Gln Ser Val Ser Ala Leu
85          90          95
Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu Val Ala Asp Ser
100          105          110
Val Leu Ser Asp Ala Ile Cys Arg Phe Leu Asp Gly Lys Leu Lys Asn
115          120          125
Tyr Arg Glu Tyr Tyr Leu Pro Tyr Leu Glu Ala Trp Leu Lys Asp Gly
130          135          140
Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln Leu Val Lys
145          150          155          160
Tyr Phe Glu Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu Gly Gly Ser
165          170          175
Leu Ala Arg Asn Asn Ala Gln Ile Leu Leu Leu Pro Tyr Phe Cys Ala
180          185          190
Ser Cys Lys Cys Gln Leu Leu Leu Arg Asp Ala Val Gln Tyr Glu
195          200          205
Glu Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg Ser Glu Leu
210          215          220
Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr Tyr Glu Arg
225          230          235          240
Leu Lys Cys Lys Ile Ala Glu Tyr Thr Asp Tyr Cys Glu Tyr Trp Tyr
245          250          255
Gln Ala Gly Leu Asn Gln Ile Lys Gln Ala Gly Thr Gly Ala Asp Thr
260          265          270
Trp Ala Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Thr Val Leu
275          280          285
Asp Ile Ile Ala Ile Phe Gln Thr Tyr Asp Phe Lys Lys Tyr Pro Leu
290          295          300
Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Pro Val Gly
305          310          315          320
Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Lys Tyr Trp Thr Gly Ala Phe
325          330          335
Asn Thr Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp
340          345          350
Leu Arg Ser Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg Tyr Phe Ser
355          360          365
Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Thr Gly Asn Gly
370          375          380
Asn Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu Arg Asp Ile
385          390          395          400
Ser Phe Pro Asn Ser Asp Ile Phe Lys Ile Glu Ser Lys Ala Ile Met
405          410          415
Asn Leu Val Gly Glu Ile Asn Ala Arg Pro Glu Tyr Arg Val Ser Arg
420          425          430
Ala Glu Phe Ser Glu Ser Thr Ala Phe Ile Tyr Leu Tyr Asp Ala Gly
435          440          445
Asn Ser Gly Leu Ser Ser Met Thr Ile Thr Ser Lys Leu Pro Gly Ile
450          455          460
Lys Asn Pro Glu Pro Ser Tyr Arg Asp Tyr Ser His Arg Leu Ser Asn
465          470          475          480
Ala Ala Cys Val Gly Ala Gly Asn Ser Arg Ile Asn Val Tyr Gly Trp
485          490          495
Thr His Thr Ser Met Ser Lys Tyr Asn Leu Ile Tyr Pro Asp Lys Ile
500          505          510
Thr Gln Ile Pro Ala Val Lys Ala Phe Asp Ile Ser Asp Thr Gly Pro
515          520          525
Gly Gln Val Ile Ala Gly Pro Gly His Thr Gly Gly Asn Val Val Ser
530          535          540
Leu Pro Tyr Tyr Ser Arg Leu Lys Ile Arg Leu Ile Pro Ala Ser Thr
545          550          555          560
Asn Lys Asn Tyr Leu Val Arg Val Arg Tyr Thr Ser Thr Ser Asn Gly
565          570          575
Arg Leu Leu Val Glu Arg Trp Ser Pro Ser Ser Ile Ile Asn Ser Tyr
580          585          590
Phe Phe Leu Pro Ser Thr Gly Pro Gly Asp Ser Phe Gly Tyr Val Asp

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595 600 605
 Thr Leu Val Thr Thr Phe Asn Gln Pro Gly Val Glu Ile Ile Ile Gln
 610 615 620
 Asn Leu Asp Thr Pro Ile Asn Val Asp Lys Val Glu Phe Ile Pro Val
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 Gln Asp Val Val Asn Asp Leu Phe Val Lys
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 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 52
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 Tyr Glu Ile Asp Gln Ala Ala Ile Ser Ile Glu Cys Met Ser Asp Glu
 20 25 30
 His Ser Pro Lys Glu Lys Met Met Leu Trp Asp Glu Val Lys Arg Ala
 35 40 45
 Lys Leu Leu Ser Gln Ser Arg Asn Leu Leu Gln Asn Gly Asp Phe Gly
 50 55 60
 Asp Phe Tyr Gly Asn Asp Trp Lys Phe Gly Asn Asn Ile Ile Ile Gly
 65 70 75 80
 Ser Asn Asn Ser Ile Phe Lys Gly Asn Phe Leu Gln Met Ser Gly Ala
 85 90 95
 Arg Asp Ile Tyr Gly Thr Ile Phe Pro Thr Tyr Ile Tyr Gln Lys Ile
 100 105 110
 Asp Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Arg Val Arg Gly Phe
 115 120 125
 Val Gly Ser Ser Lys Asp Leu Arg Leu Met Val Thr Arg Tyr Gly Lys
 130 135 140
 Glu Ile Asp Ala Met Met Asn Val Pro Asn Asp Leu Ala Tyr Met Gln
 145 150 155 160
 Pro Asn Pro Ser Cys Gly Asp Ser Arg Cys Glu Ser Ser Ser Gln Tyr
 165 170 175
 Val Ser Gln Gly Tyr Pro Thr Pro Thr Asp Gly Tyr Ala Pro Asp Arg
 180 185 190
 Tyr Ala Cys Pro Ser Ser Ser Asp Lys Lys His Val Met Cys His Asp
 195 200 205
 Arg His Pro Phe Asp Phe His Ile Asp Thr Gly Glu Leu Asp Thr Asn
 210 215 220
 Thr Asn Val Gly Ile Asp Val Leu Phe Lys Ile Ser Asn Pro Asp Gly
 225 230 235 240
 Tyr Ala Thr Leu Gly Asn Leu Glu Val Ile Glu Glu Gly Pro Leu Thr
 245 250 255
 Gly Glu Ala Leu Thr His Val Lys Gln Lys Glu Lys Lys Trp Lys Gln
 260 265 270
 His Met Glu Lys Lys Arg Trp Glu Thr Gln Gln Ala Tyr Asp Pro Ala
 275 280 285
 Lys Gln Ala Val Asp Thr Leu Phe Thr Asn Glu Gln Glu Leu His Tyr
 290 295 300
 His Ile Thr Leu Asp Tyr Ile Gln Thr Leu Ile Asp Trp Tyr Ser Arg
 305 310 315 320
 Phe Pro Ile Tyr Thr Met Thr Gly Tyr Arg Asp Ala Pro Gly Met Asn
 325 330 335
 Tyr Asp Gly Tyr Gln Gly Leu Asn Ala Arg Ile Met Gln Ala Tyr Asn
 340 345 350
 Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp Phe Thr Lys Gly
 355 360 365
 Leu Gln Gly Trp His Ala Ala Gly Lys Ala Ala Val Gln Gln Ile Asp
 370 375 380
 Gly Ala Ser Val Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln
 385 390 395 400
 Asn Leu His Ala Gln Asp His His Gly Tyr Met Leu Arg Val Ile Ala

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